OM nucleic - nucleic search, using sw model

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GenCore version 5.1.7

Run on: February 7, 2006, 11:06:42 ; Search time 135 seconds
                                              (without alignments)
                                            329.178 Million cell updates/sec

Title: US-10-613-390B-1
Perfect score: 25
Sequence: 1 tattaaggggcctggccccctaata 25
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 1427136

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents NA:*
                1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                8: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*
                9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	17.4	69.6	25	3	US-09-396-196G-116728	Sequence 116728, App
c 2	15.8	63.2	25	3	US-09-396-196G-116728	Sequence 116728, App
c 3	14.8	59.2	25	3	US-09-396-196G-86335	Sequence 86335, A
c 4	14.8	59.2	25	3	US-09-396-196G-86336	Sequence 86336, A
c 5	14.4	57.6	70	2	US-08-434-001-117	Sequence 117, App
c 6	14.4	57.6	70	2	US-08-433-585-117	Sequence 117, App
c 7	14.4	57.6	70	2	US-08-434-425-117	Sequence 117, App
c 8	14.4	57.6	70	2	US-08-437-667-117	Sequence 117, App
c 9	14.4	57.6	70	2	US-08-906-955-117	Sequence 117, App
c 10	14.4	57.6	70	3	US-08-945-909-117	Sequence 117, App
c 11	14.4	57.6	70	3	US-09-396-002A-117	Sequence 117, App
c 12	14.4	57.6	70	3	US-09-396-002A-117	Sequence 117, App
c 13	14.4	57.6	6	6	PCT-US96-06060-117	Sequence 26177, App
c 14	14.4	57.6	25	3	US-09-396-196G-26177	Sequence 26177, A
c 15	14.2	56.8	49	2	US-08-171-389-405	Sequence 405, App
c 16	14.2	56.8	49	2	US-08-171-389-405	Sequence 405, App
c 17	14.2	56.8	49	2	US-08-123-936-405	Sequence 405, App
c 18	14.2	56.8	49	2	US-08-123-936-405	Sequence 405, App
c 19	14.2	56.8	49	2	US-08-475-228A-405	Sequence 405, App
c 20	14.2	56.8	49	2	US-08-475-228A-405	Sequence 405, App
c 21	14.2	56.8	49	2	US-08-482-080A-405	Sequence 405, App
c 22	14.2	56.8	49	3	US-08-482-080A-405	Sequence 405, App
c 23	14.2	56.8	49	3	US-09-354-947-405	Sequence 405, App
c 24	14.2	56.8	49	3	US-09-354-947-405	Sequence 405, App
c 25	14.2	56.8	49	3	US-09-354-947-405	Sequence 405, App
c 26	14.2	56.8	49	3	US-09-993-346-405	Sequence 405, App
c 27	14.2	56.8	49	6	US-09-993-346-405	Sequence 405, App
c 28	14.2	56.8	49	6	PCT-US93-12388-405	Sequence 405, App
c 29	14	56.0	63	3	US-09-508-516-4	Sequence 4, Appli
c 30	13.8	55.2	61	3	US-09-513-999C-15155	Sequence 15155, A
c 31	13.4	53.6	50	3	US-10-131-827-7211	Sequence 7211, Ap
c 32	13.4	53.6	51	2	US-09-443-199C-1033	Sequence 1033, Ap
c 33	13.4	53.6	67	2	US-07-977-284A-245	Sequence 245, App
c 34	13.4	53.6	67	2	US-08-256-426B-245	Sequence 245, App
c 35	13.4	53.6	68	3	US-09-513-999C-23652	Sequence 23652, A
c 36	13.4	53.6	83	3	US-09-513-999C-8355	Sequence 8355, Ap
c 37	13.2	52.8	25	3	US-09-621-976-22105	Sequence 22105, A
c 38	13.2	52.8	25	3	US-09-396-196G-22105	Sequence 22105, A
c 39	13.2	52.8	25	3	US-09-396-196G-86335	Sequence 86335, A
c 40	13.2	52.8	25	3	US-09-396-196G-86336	Sequence 86336, A
c 41	13.2	52.8	28	2	US-09-396-196G-86391	Sequence 86391, A
c 42	13.2	52.8	28	2	US-08-331-394-46	Sequence 46, Appl
c 43	13.2	52.8	28	2	US-08-250-858-46	Sequence 46, Appl
c 44	13.2	52.8	28	2	US-08-250-858-46	Sequence 46, Appl
c 45	13.2	52.8	28	2	US-08-446-915-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-396-196G-116728/c
; Sequence 116728, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116728
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-116728

Query Match   69.6%; Score 17.4; DB 3; Length 25;
Best Local Similarity   94.7%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   6 AGGGGCCTGGCCCCCTTAAT 24
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Db   25 AGGGGCCTGGCCACCTTAAT 7

RESULT 2
US-09-396-196G-116728
; Sequence 116728, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

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;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
;   SEQ ID NO 116728
;     LENGTH: 25
;     TYPE: DNA
;     ORGANISM: mus musculus

Qy                US-09-396-196G-116728

Db                US-09-396-196G-116728

Query Match     63.2%;  Score 15.8;  DB 3;  Length 25;
Best Local Similarity   89.5%;
Matches  17;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy          2  ATTPAAGGGGCCCTGGCCCCT  20
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Db          7  ATTPAAGGTGCCAGGCCCCT   25
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RESULT 3
US-09-396-196G-86335
; Sequence 86335, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Mittman
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09,396,196G
;   CURRENT FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
;   SEQ ID NO 86335
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus

Qy   US-09-396-196G-86335

Db   US-09-396-196G-86335

Query Match   59.2%; Score 14.8; DB 3; Length 25;
Best Local Similarity   88.9%;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   5 AAGGGGCCCTGGCCCCTTA 22
               ||| ||||||||||| ||||
Db   7 AAGAGGCCTGGCCACTTA 24

RESULT 4
US-09-396-196G-86336
; Sequence 86336, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Mittman
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09,396,196G
;   CURRENT FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
;   SEQ ID NO 86336
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus

Qy   US-09-396-196G-86336

Db   US-09-396-196G-86336

Query Match   59.2%; Score 14.8; DB 3; Length 25;

Best Local Similarity   88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   5 AAGGGGCCCTGGCCCCTTA 22
               ||| ||||||||||| ||||
Db   1 AAGAGGCCTGGCCACTTA 18

RESULT 5
US-08-434-001-117/c
; Sequence 117, Application US/08434001
; Patent No. 5712375
; GENERAL INFORMATION:
;   APPLICANT: JENSEN, KIRK
;   APPLICANT: -CHEN, HANG
;   APPLICANT: MORRIS, KEVIN
;   APPLICANT: STEPHENS, ANDREW
;   APPLICANT: GOLD, LARRY
;   TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
;   TITLE OF INVENTION: EXPONENTIAL ENRICYMENT: TISSUE
;   TITLE OF INVENTION: SELEX
;   NUMBER OF SEQUENCES: 235
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Swanson & Bratschun, L.L.C.
;   STREET: 8400 E. Prentice Avenue, Suite 200
;   CITY: Englewood
;   STATE: Colorado
;   COUNTRY: USA
;   ZIP: 80111
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;   COMPUTER: IBM pc compatible
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/434,001
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/714,131
;   FILING DATE: 10-JUNE-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/536,428
;   FILING DATE: 11-JUNE-1990
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/964,624
;   FILING DATE: 21-OCTOBER-1992
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Barry J. Swanson
;   REGISTRATION NUMBER: 33,215
;   REFERENCE/DOCKET NUMBER: NEX30.3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (303) 793-3333
;   TELEFAX: (303) 793-3433
;   INFORMATION FOR SEQ ID NO: 117:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 70 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear

Qy   US-08-434-001-117

Db   US-08-434-001-117

Query Match   57.6%; Score 14.4; DB 2; Length 70,;
Best Local Similarity   75.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy   2 ATTPAAGGGGGCCTGGCCCCCTTAATA 25
               ||||| |||||||| |||||| ||||
Db   60 AATPAAGCGGCGCCTGGGAGCTTTAACA 37

RESULT 6
US-08-433-585-117/c
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; Sequence 117, Application US/08433585
; Patent No. 5763566
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
; NUMBER OF SEQUENCES: 235
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,585
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-433-585-117

Query Match     57.6%;  Score 14.4;  DB 2;  Length 70;
Best Local Similarity   75.0%;  Pred. No. 7.3e+02;
Matches 18;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

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Qy    2 ATTAAGGGGGCCTGGCCCCTTAATA 25
          |||||||||||| |||||||| || |
Db   60 AATAAGCGGGCCTGGAGCTTTAACA 37
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RESULT 7
US-08-434-425-117/c
; Sequence 117, Application US/08434425
; Patent No. 5789157
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE

; TITLE OF INVENTION: SELEX
; NUMBER OF SEQUENCES: 235
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,425
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-434-425-117

Query Match   57.6%; Score 14.4; DB 2; Length 70;
Best Local Similarity   75.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy    2 ATTAAGGGGGCCTGGCCCCTTAATA 25
          ||||| |||||||||||||||| || |
Db   60 AATAAGCGGGCCTGGAGCTTTAACA 37
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RESULT 8
US-08-437-667-1117/c
; Sequence 117, Application US/08437667
; Patent No. 5864026
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
; NUMBER OF SEQUENCES: 235
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:

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;   MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;   COMPUTER: IBM pc compatible
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: WordPerfect 5.1
;   APPLICATION NUMBER: US/08/437,667
;   CLASSIFICATION: 435
; CURRENT APPLICATION DATA:
;   FILING DATE:
;   APPLICATION NUMBER: US/08/437,667
; PRIOR APPLICATION DATA:
;   FILING DATE:
;   APPLICATION NUMBER: 07/964,624
;   FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/536,428
;   FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/714,131
;   FILING DATE: 10-JUNE-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Barry J. Swanson
;   REGISTRATION NUMBER: 33,215
;   REFERENCE/DOCKET NUMBER: NEX30.2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (303) 793-3333
;     TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 117:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 70 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear

US-08-437-667-117

Qy   2 ATTAAGGGGGCCTCGGCCCCCTTAATA 25
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Db  60 AATAAGCCGGCCTGGGAGCTTTAACA 37

Query Match          57.6%;  Score 14.4;  DB 2;  Length 70;
Best Local Similarity 75.0%;  Pred. No. 7.3e+02;
Matches 18;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;
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```
RESULT 9
US-08-906-955-1117/c
Sequence 117, Application US/0890695
Patent No. 6013443
; GENERAL INFORMATION:
;   APPLICANT: HEILIG, JOSEPH S.
;   APPLICANT: GOLD, LARRY
;   TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
;   TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
;   TITLE OF INVENTION: SELEX
;   NUMBER OF SEQUENCES: 240
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Swanson & Bratschun, L.L.C.
;     STREET: 8400 E. Prentice Avenue, Suite 200
;     CITY: Englewood
;     STATE: Colorado
;     COUNTRY: USA
;     ZIP: 80111
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;     COMPUTER: IBM pc compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/906,955
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/714,131
;     FILING DATE: 10-JUNE-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/434,001
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RESULT 10
US-08-945-909-1117/c
Sequence 117, Application US/08945909
Patent No. 6114120
; GENERAL INFORMATION:
;   APPLICANT: JENSEN, KIRK
;   APPLICANT: CHEN, HANG
;   APPLICANT: MORRIS, KEVIN
;   APPLICANT: STEPHENS, ANDREW
;   APPLICANT: GOLD, LARRY
;   TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS
;   TITLE OF INVENTION: ENRICHMENT: TISSUE SELEX
;   NUMBER OF SEQUENCES: 240
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Swanson & Bratschun, L.L.C.
;     STREET: 8400 E. Prentice Avenue, Suite 200
;     CITY: Englewood
;     STATE: Colorado
;     COUNTRY: USA
;     ZIP: 80111
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;     COMPUTER: IBM pc compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: WordPerfect 6.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/945,909
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/434,001
;     FILING DATE: 03-MAY-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/434,425
;     FILING DATE: 03-MAY-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/437,667
;     FILING DATE: 03-MAY-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/434,001
;     FILING DATE: 03-MAY-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US96/06060
;     FILING DATE: 01-MAY-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/433,585
;     FILING DATE: 03-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Barry J. Swanson
;     REGISTRATION NUMBER: 33,215
;     REFERENCE/DOCKET NUMBER: NEX30C-US
;   FILING DATE: 05-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Barry J. Swanson
;     REGISTRATION NUMBER: 33,215
;     REFERENCE/DOCKET NUMBER: NEX30-5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (303) 793-3333
;       TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 117:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 70 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear

US-08-906-955-117

Qy   2 ATTAAGGGGGCCTCGGCCCCCTTAATA 25
          ||||| |||||||||| ||||||
Db  60 AATAAGCCGGCCTGGGAGCTTTAACA 37

Query Match          57.6%;  Score 14.4;  DB 3;  Length 70;
Best Local Similarity 75.0%;  Pred. No. 7.3e+02;
Matches 18;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;
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```
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (303) 793-3333
;     TELEFAX: (303) 793-3433
;  INFORMATION FOR SEQ ID NO: 117:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 70 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
US-08-945-909-117

Qy          2 ATTAAGGGGGCCTGGCCCCCTTAATA 25
              | ||| ||||| ||||||| | |||| |
Db         60 AATAAGCGGCCTGGAGCTTTAACA 37
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Query Match   57.6%; Score 14.4; DB 3; Length 70;
Best Local Similarity   75.0%; Pred. No. 7.3e+02;
Matches   18; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

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RESULT 11
US-09-396-002A-117/c
Sequence 117, Application US/0939600A
Patent No. 6376474
;  GENERAL INFORMATION:
;     APPLICANT: HEILIG, JOSEPH S.
;                GOLD, LARRY
;  TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
;                EXPONENTIAL ENRICHMENT: TISSUE SELEX
;  NUMBER OF SEQUENCES: 240
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Swanson & Bratschun, L.L.C.
;     STREET: 1745 Shea Center Drive, Suite 330
;     CITY: Highlands Ranch
;     STATE: Colorado
;     COUNTRY: USA
;     ZIP: 80129
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;     COMPUTER: IBM pc compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: WordPerfect 8.0
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/396,002A
;     FILING DATE: 14-Sep-1999
;     CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/714,131
;     FILING DATE: 10-JUNE-1991
;     APPLICATION NUMBER: 08/434,001
;     FILING DATE: 05-MAY-1995
;     APPLICATION NUMBER: 08/906,955
;     FILING DATE: 05-AUGUST-1997
;  ATTORNEY/AGENT INFORMATION:
;     NAME: Barry J. Swanson
;     REGISTRATION NUMBER: 33,215
;     REFERENCE/DOCKET NUMBER: NEX30-5/D
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (303) 268-0066
;     TELEFAX: (303) 268-0065
;  INFORMATION FOR SEQ ID NO: 117:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 70 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;     SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-09-396-002A-117
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Query Match   57.6%; Score 14.4; DB 3; Length 70;
Best Local Similarity   75.0%; Pred. No. 7.3e+02;
Matches   18; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

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Qy          2 ATTAAGGGGGCCTGGCCCCCTTAATA 25
              | ||| ||||| ||||||| | |||| |
Db         60 AATAAGCGGCCTGGAGCTTTAACA 37

RESULT 12
US-10-077-319-117/c
Sequence 117, Application US/10077319
Patent No. 6613526
;  GENERAL INFORMATION:
;     APPLICANT: HEILIG, JOSEPH S.
;                GOLD, LARRY
;  TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
;                EXPONENTIAL ENRICHMENT: TISSUE SELEX
;  NUMBER OF SEQUENCES: 240
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Swanson & Bratschun, L.L.C.
;     STREET: 1745 Shea Center Drive, Suite 330
;     CITY: Highlands Ranch
;     STATE: Colorado
;     COUNTRY: USA
;     ZIP: 80129
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;     COMPUTER: IBM pc compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: WordPerfect 8.0
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/077,319
;     FILING DATE: 14-Feb-2002
;     CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/396,002
;     FILING DATE: 14-Sep-1999
;     APPLICATION NUMBER: 07/714,131
;     FILING DATE: 10-JUNE-1991
;     APPLICATION NUMBER: 08/434,001
;     FILING DATE: 05-MAY-1995
;     APPLICATION NUMBER: 08/906,955
;     FILING DATE: 05-AUGUST-1997
;  ATTORNEY/AGENT INFORMATION:
;     NAME: Barry J. Swanson
;     REGISTRATION NUMBER: 33,215
;     REFERENCE/DOCKET NUMBER: NEX30-5/D
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (303) 268-0066
;     TELEFAX: (303) 268-0065
;  INFORMATION FOR SEQ ID NO: 117:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 70 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;     SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-10-077-319-117
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Query Match   57.6%; Score 14.4; DB 3; Length 70;
Best Local Similarity   75.0%; Pred. No. 7.3e+02;
Matches   18; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

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Qy          2 ATTAAGGGGGCCTGGCCCCCTTAATA 25
              | ||| ||||| ||||||| | |||| |
Db         60 AATAAGCGGCCTGGAGCTTTAACA 37

RESULT 13
PCT-US96-06060-117/c
Sequence 117, Application PC/TUS9606060
;  GENERAL INFORMATION:
;     APPLICANT: JENSEN, KIRK
;     APPLICANT: CHEN, HANG
;     APPLICANT: MORRIS, KEVIN
;     APPLICANT: STEPHENS, ANDREW
```

APPLICANT: GOLD, LARRY
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
TITLE OF INVENTION: SELEX
NUMBER OF SEQUENCES: 240
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06060
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,425
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/437,667
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,585
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,001
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX30/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

RESULT 14
US-09-396-196G-26177
Sequence 26177, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack

Qy
Db

Query Match   57.6%; Score 14.4; DB 6; Length 70;
Best Local Similarity   75.0%;   Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy  2 ATTAAGGGGGCCTGGGCCCCTTAATA 25
        |||||| |||| |||| |||||||
Db 60 AATAAGCGGCCGCCTGGAGCTTTAACA 37
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APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: US/09/396,196G
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26177
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-26177

Qy
Db

Query Match   56.8%; Score 14.2; DB 3; Length 25;
Best Local Similarity   84.2%;   Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 3 TTAAGGGGGCCTGGGCCCCTT 21
       |||||||| ||||| ||||
Db 1 TTACGGGTCCTGGGCCACCTT 19
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RESULT 15
US-08-171-389-405
Sequence 405, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

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;  INFORMATION FOR SEQ ID NO: 405:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  49 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human adenosine deaminase gene
US-08-171-389-405
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Query Match        56.8%;  Score 14.2;  DB 2;  Length 49;
Best Local Similarity   84.2%;  Pred. No. 8.7e+02;
Matches  16;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy      7 GGGGCCTGGGCCCCTTAATA 25
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Db     10 GGGGGCCCGGCGCCCGTTAAGA 28
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Search completed: February 7, 2006, 12:09:00
Job time : 136 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 12:09:14 ; Search time 406 seconds
                 (without alignments)
                 51.606 Million cell updates/sec

Title: US-10-613-390B-1
Perfect score: 25
Sequence: 1 tattaagggggcctggcccctaata 25
Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 6068529 seqs, 419036697 residues
Total number of hits satisfying chosen parameters: 11614816

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_NA_New:*
                 1: /cgn2_6/ptcodata/2/pubpna/US08_NEW_PUB.seq:*
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                 6: /cgn2_6/ptcodata/2/pubpna/US10_NEW_PUB.seq:*
                 7: /cgn2_6/ptcodata/2/pubpna/US11_NEW_PUB.seq:*
                 8: /cgn2_6/ptcodata/2/pubpna/US11_NEW_PUB.seq1:*
                 9: /cgn2_6/ptcodata/2/pubpna/US11_NEW_PUB.seq2:*
                 10: /cgn2_6/ptcodata/2/pubpna/US11_NEW_PUB.seq3:*
                 11: /cgn2_6/ptcodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
c 1	16	64.0	23	7	US-10-310-914A-1296097	Sequence 1296097,
c 2	15.8	63.2	21	7	US-10-310-914A-621697	Sequence 621697,
c 3	15.4	61.6	21	7	US-10-310-914A-679212	Sequence 679212,
c 4	15.4	61.6	24	7	US-10-310-914A-679219	Sequence 679219,
c 5	15	60.0	19	7	US-11-121-849-627249	Sequence 627249,
c 6	15	60.0	25	8	US-10-310-914A-42167	Sequence 42167, A
c 7	14.8	59.2	25	8	US-10-310-914A-760090	Sequence 760090,
c 8	14.6	58.4	25	8	US-11-121-849-615428	Sequence 615428,
c 9	14.4	57.6	18	7	US-10-310-914A-1160660	Sequence 1160660,
c 10	14.4	57.6	20	7	US-10-310-914A-236069	Sequence 236069,
c 11	14.4	57.6	21	7	US-10-310-914A-535246	Sequence 535246,
c 12	14.4	57.6	25	8	US-11-121-849-535269	Sequence 535269,
c 13	14.4	57.6	23	7	US-10-310-914A-1296097	Sequence 1296097,
c 14	14.4	57.6	26	7	US-11-121-849-1153244	Sequence 1153244,
c 15	14.2	56.8	19	9	US-11-101-244-1315095	Sequence 1315095,
c 16	14.2	56.8	19	10	US-11-083-784-1315095	Sequence 1315095,
c 17	14.2	56.8	21	7	US-10-310-914A-621697	Sequence 621697,
c 18	14.2	56.8	22	7	US-10-310-914A-1192905	Sequence 1192905,
c 19	14.2	56.8	25	8	US-11-121-849-518737	Sequence 518737,
c 20	14.2	56.8	25	8	US-11-121-849-518738	Sequence 518738,
c 21	13.8	55.2	19	7	US-10-310-914A-990748	Sequence 990748,
c 22	13.8	55.2	21	7	US-10-310-914A-679212	Sequence 679212,
c 23	13.8	55.2	23	7	US-10-310-914A-860902	Sequence 860902,
c 24	13.8	55.2	24	7	US-10-310-914A-679219	Sequence 679219,
c 25	13.8	55.2	25	7	US-10-310-914A-1325744	Sequence 1325744,
c 26	13.8	55.2	25	8	US-11-121-849-28266	Sequence 28266, A
c 27	13.8	55.2	25	8	US-11-121-849-38739	Sequence 38739, A
c 28	13.8	55.2	25	7	US-11-121-849-299363	Sequence 299363,
c 29	13.8	55.2	25	8	US-10-310-914A-299364	Sequence 299364,
c 30	13.8	55.2	25	8	US-10-310-914A-299365	Sequence 299365,
c 31	13.8	55.2	25	7	US-11-121-849-450067	Sequence 450067,
c 32	13.8	55.2	25	8	US-11-121-849-514431	Sequence 514431,
c 33	13.8	55.2	25	8	US-11-136-527-260490	Sequence 260490,
c 34	13.8	55.2	25	8	US-11-136-527-260490	Sequence 260502,
c 35	13.8	54.4	25	8	US-10-310-914A-299906	Sequence 299906,
c 36	13.6	54.4	25	8	US-11-136-527-299906	Sequence 260502,
c 37	13.6	54.4	20	7	US-10-310-914A-915730	Sequence 915730,
c 38	13.6	54.4	22	7	US-10-310-914A-1053611	Sequence 1053611,
c 39	13.6	54.4	25	7	US-10-310-914A-1117125	Sequence 1117125,
c 40	13.6	54.4	25	7	US-10-310-914A-95810	Sequence 95810, A
c 41	13.6	54.4	25	8	US-10-310-914A-713535	Sequence 713535, A
c 42	13.6	54.4	25	8	US-11-121-849-95350	Sequence 95350, A
c 43	13.6	54.4	25	7	US-11-121-849-292815	Sequence 292815,
c 44	13.6	54.4	25	8	US-11-121-849-442329	Sequence 442329,
c 45	13.6	54.4	25	8	US-11-121-849-613025	Sequence 613025,

ALIGNMENTS

RESULT 1
US-10-310-914A-1296097/c
; Sequence 1296097, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; FILE REFERENCE: 06087.0200.CPUSO1
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1296097
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1296097

Query Match   64.0%; Score 16; DB 7; Length 23;
Best Local Similarity   100.0%; Pred. No. 1.5e+02;
Matches   16; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   5 AAGGGGCCTTGGCCCCT 20
              |||||||||||||||||
Db   23 AAGGGGCCTTGGCCCCT 8

RESULT 2
US-10-310-914A-621697
; Sequence 621697, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; FILE REFERENCE: 06087.0200.CPUSO1
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 621697
; LENGTH: 21

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;      TYPE: RNA
;      ORGANISM: Human
US-10-310-914A-621697

Qy       5 AAGGGGCCTCGGCCCCTTAA 23
             ||  ||||||||||:: ||
Db       1 AAGAGGCCTUGGCCCCUCAA 19
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RESULT 3
US-10-310-914A-679212/c
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;   Sequence 679212, Application US/10310914A
;   Publication No. US20060003322A1
;   GENERAL INFORMATION:
;      APPLICANT: Bentwich, Isaac
;      APPLICANT: Shiler, Kvuzat
;      TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;      TITLE OF INVENTION:  uses thereof
;      FILE REFERENCE: 06087.0200.CPUS01
;      CURRENT APPLICATION NUMBER: US/10/310,914A
;      CURRENT FILING DATE: 2002-12-06
;      NUMBER OF SEQ ID NOS: 1388402
;      SOFTWARE: Patentin version 3.3
;      SEQ ID NO 679212
;      LENGTH: 21
;      TYPE: RNA
;      ORGANISM: Human
US-10-310-914A-679212
```

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  Query Match             61.6%;  Score 15.8;  DB 7;  Length 21;
  Best Local Similarity   78.9%;
  Matches   15;  Conservative   2;  Mismatches   2;  Indels   0;  Gaps   0;
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RESULT 4
US-10-310-914A-679219/c
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;   Sequence 679219, Application US/10310914A
;   Publication No. US20060003322A1
;   GENERAL INFORMATION:
;      APPLICANT: Bentwich, Isaac
;      APPLICANT: Shiler, Kvuzat
;      TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;      TITLE OF INVENTION:  uses thereof
;      FILE REFERENCE: 06087.0200.CPUS01
;      CURRENT APPLICATION NUMBER: US/10/310,914A
;      CURRENT FILING DATE: 2002-12-06
;      NUMBER OF SEQ ID NOS: 1388402
;      SOFTWARE: Patentin version 3.3
;      SEQ ID NO 679219
;      LENGTH: 24
;      TYPE: RNA
;      ORGANISM: Human
US-10-310-914A-679219
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```
  Query Match             61.6%;  Score 15.4;  DB 7;  Length 24;
  Best Local Similarity   94.1%;
  Matches   16;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy       4 TAAGGGGCCTGGCCCCT 20
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Db      21 TAAGGGGCCTGGCCACT 5
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RESULT 5
US-10-310-914A-627249
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Qy       4 TAAGGGGCCTGGCCCCT 20
             |||||||||||||| ||
Db      19 TAAGGGGCCTGGCCACT 3
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;   Sequence 627249, Application US/10310914A
;   Publication No. US20060003322A1
;   GENERAL INFORMATION:
;      APPLICANT: Bentwich, Isaac
;      APPLICANT: Shiler, Kvuzat
;      TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;      TITLE OF INVENTION:  uses thereof
;      FILE REFERENCE: 06087.0200.CPUS01
;      CURRENT APPLICATION NUMBER: US/10/310,914A
;      CURRENT FILING DATE: 2002-12-06
;      NUMBER OF SEQ ID NOS: 1388402
;      SOFTWARE: Patentin version 3.3
;      SEQ ID NO 627249
;      LENGTH: 19
;      TYPE: RNA
;      ORGANISM: Human
US-10-310-914A-627249
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  Query Match             60.0%;  Score 15;  DB 7;  Length 19;
  Best Local Similarity   86.7%;
  Matches   13;  Conservative   2;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       6 AGGGGCCTGGCCCCT 20
             |||||||||||||:
Db       5 AGGGGCCUGGCCCCU 19
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RESULT 6
US-11-121-849-42167
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;   Sequence 42167, Application US/11121849
;   Publication No. US20050272080A1
;   GENERAL INFORMATION:
;      APPLICANT: John Palma
;      TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
;      TITLE OF INVENTION:  Microarrays
;      FILE REFERENCE: 3684.1
;      CURRENT APPLICATION NUMBER: US/11/121,849
;      PRIOR APPLICATION NUMBER: 60/567,949
;      PRIOR FILING DATE: 2004-05-03
;      CURRENT FILING DATE: 2005-05-03
;      NUMBER OF SEQ ID NOS: 673904
;      SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;      SEQ ID NO 42167
;      LENGTH: 25
;      TYPE: DNA
;      ORGANISM: Homo sapien
US-11-121-849-42167
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```
  Query Match             60.0%;  Score 15;  DB 8;  Length 25;
  Best Local Similarity   78.3%;
  Matches   18;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;

Qy       1 TATTAAGGGGCCTGGCCCCTTAA 23
             ||||||||| |||||||||||:
Db       1 TATAAAGGGGCTCTGCCCCTTTAA 23
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RESULT 7
US-10-310-914A-760090/c
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;   Sequence 760090, Application US/10310914A
;   Publication No. US20060003322A1
;   GENERAL INFORMATION:
;      APPLICANT: Bentwich, Isaac
;      APPLICANT: Shiler, Kvuzat
;      TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
;      TITLE OF INVENTION:  uses thereof
;      FILE REFERENCE: 06087.0200.CPUS01
;      CURRENT APPLICATION NUMBER: US/10/310,914A
;      CURRENT FILING DATE: 2002-12-06
;      NUMBER OF SEQ ID NOS: 1388402
;      SOFTWARE: Patentin version 3.3
;      SEQ ID NO 760090
;      LENGTH: 25
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; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-760090

Query Match   59.2%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   6 AGGGGGCCTGGCCCCCTTAA 23
         ||||||||||||||| | .
Db 22 AGGGGGCCTGGCCCCCTCA 5

RESULT 8
US-11-121-849-615428/c
Sequence 615428, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded s
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 615428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-615428

Query Match   58.4%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   5 AAGGGGCCTGGCCCCCTTAATA 25
         || |||||||||||| |||| |
Db 25 ACGGTGCCTGGCCTCTTATTA 5

RESULT 9
US-10-310-914A-1160660
Sequence 1160660, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1160660
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1160660

Query Match   57.6%; Score 14.4; DB 7; Length 18;
Best Local Similarity 75.0%; Pred. No. 8.1e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GCCTGGCCCCCTTAATA 25
         |||.||||||||| ||:|
Db   2 GCCTGGCCCCCUCAUA 17

RESULT 10

US-10-310-914A-236069
; Sequence 236069, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 236069
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-236069

Query Match   57.6%; Score 14.4; DB 7; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GCCTGGCCCCCTTAATA 25
         ||||||||||||||||
Db 16 GCCTGGCCCCCTTAACA 1

RESULT 11
US-10-310-914A-535246
Sequence 535246, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 535246
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-535246

Query Match   57.6%; Score 14.4; DB 7; Length 21;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 1; Gaps 0;

Qy   5 AAGGGGCCCTGGCCCCCT 20
         |||||||||||||||:|
Db   4 AAGAGGCCTGGCCCCU 19

RESULT 12
US-10-310-914A-535269
Sequence 535269, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 535269
; LENGTH: 21

```
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-535269

Query Match             57.6%;  Score 14.4;  DB 7;  Length 21;
Best Local Similarity   81.2%;  Pred. No. 8.1e+02;
Matches    13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 AAGGGGCCTGGCCCCT 20
                ||| ||||||||||:
Db          6 AAGAGGCCUGGCCCCU 21
```

RESULT 13
```
US-10-310-914A-1296097
Sequence 1296097, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
;   APPLICANT: Bentwich, Isaac
;   APPLICANT: Shiler, Kvuzat
;   TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;   TITLE OF INVENTION: uses thereof
;   FILE REFERENCE: 06087.0200.CPUS01
;   CURRENT APPLICATION NUMBER: US/10/310,914A
;   CURRENT FILING DATE: 2002-12-06
;   NUMBER OF SEQ ID NOS: 1388402
;   SOFTWARE: Patentin version 3.3
;   SEQ ID NO 1296097
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-1296097

Query Match             57.6%;  Score 14.4;  DB 7;  Length 23;
Best Local Similarity   81.2%;  Pred. No. 8.2e+02;
Matches    13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 AGGGGCCTGGCCCCTT 21
                |||||| |||||::
Db          8 AGGGGCCAGGCCCCU 23
```

RESULT 14
```
US-10-310-914A-1153244/c
Sequence 1153244, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
;   APPLICANT: Bentwich, Isaac
;   APPLICANT: Shiler, Kvuzat
;   TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;   TITLE OF INVENTION: uses thereof
;   FILE REFERENCE: 06087.0200.CPUS01
;   CURRENT APPLICATION NUMBER: US/10/310,914A
;   CURRENT FILING DATE: 2002-12-06
;   NUMBER OF SEQ ID NOS: 1388402
;   SOFTWARE: Patentin version 3.3
;   SEQ ID NO 1153244
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-1153244

Query Match             57.6%;  Score 14.4;  DB 7;  Length 26;
Best Local Similarity   93.8%;  Pred. No. 8.3e+02;
Matches    15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TATTAAGGGGGCCTGGC 16
                |||| ||||||||||||
Db         21 TATTTAGGGGGCCTGGC 6
```

RESULT 15
US-11-101-244-1315095

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Sequence 1315095, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
;   APPLICANT: Dharmacon, Inc.
;   APPLICANT: Khvorova, Anastasia
;   APPLICANT: Reynolds, Angela
;   APPLICANT: Leake, Devin
;   APPLICANT: Marshall, William
;   APPLICANT: Scaringe, Stephen
;   TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;   FILE REFERENCE: 13499US
;   CURRENT APPLICATION NUMBER: US/11/101,244
;   CURRENT FILING DATE: 2005-04-07
;   PRIOR APPLICATION NUMBER: 60/502,050
;   PRIOR FILING DATE: 2003-09-10
;   PRIOR APPLICATION NUMBER: 60/426,137
;   PRIOR FILING DATE: 2002-11-14
;   NUMBER OF SEQ ID NOS: 1591911
;   SOFTWARE: Proprietary
;   SEQ ID NO 1315095
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1315095

Query Match             56.8%;  Score 14.2;  DB 9;  Length 19;
Best Local Similarity   63.2%;  Pred. No. 1e+03;
Matches    12;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 GGGGCCTGGGCCCCTTAATA 25
                |||||||||| |:|| |:|
Db          1 GGAGCCUGGGCCUCUGAUA 19

Search completed: February 7, 2006, 12:29:26
Job time : 406 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 7, 2006, 10:50:27 ; Search time 1992 Seconds
                                              (without alignments)
                                              713.397 Million cell updates/sec

Title:           US-10-613-390B-1
Perfect score:   25
Sequence:        1 tattaaggggcctggcccctaata 25

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5883141 seqs, 2842172 5653 residues
Total number of hits satisfying chosen parameters:   2525446

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                 1: gb_ba:*
                 2: gb_in:*
                 3: gb_env:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_ph:*
                 7: gb_pat:*
                 8: gb_pr:*
                 9: gb_ro:*
                 10: gb_sts:*
                 11: gb_sy:*
                 12: gb_un:*
                 13: gb_vi:*
                 14: gb_htg:*
                 15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                      SUMMARIES
Result                 %     Query
  No.   Score      Match   Length  DB    ID            Description
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c   1   15.8       63.2      51     6   CQ004908    CQ004908 Sequence
c   2   15.4       61.6      50     6   CQ006075    CQ006075 Sequence
c   3   15.4       61.6      50     6   CQ006077    CQ006077 Sequence
c   4   15.4       61.6      50     6   CQ006077    CQ006077 Sequence
c   5   14.4       57.6      70     6   AR012502    AR012502 Sequence
c   6   14.4       57.6      70     6   AR020330    AR020330 Sequence
c   7   14.4       57.6      70     6   AR109351    AR109351 Sequence
c   8   14.4       57.6      70     6   I82676      I82676 Sequence 11
c   9   14.4       57.6      70     6   AR368542    AR368542 Sequence
c  10   14.4       57.6      70     6   AR391734    AR391734 Sequence
c  11   14.4       57.6      74     5   AY266911    AY266911 Gadus mor
c  12   14.4       57.6      74     5   AY266914    AY266914 Gadus mor
c  13   14.4       57.6      74     5   AY266915    AY266915 Gadus mor
c  14   14.4       57.6      74     5   AY266916    AY266916 Gadus mor
c  15   14.4       57.6      74     5   AY266917    AY266917 Gadus mor
c  16   14.4       57.6      74     5   AY266918    AY266918 Gadus mor
c  17   14.4       57.6      74     5   AY266920    AY266920 Gadus mor
c  18   14.2       57.6      74     5   AY266922    AY266922 Gadus mor
c  19   14.4       57.6      74     5   AY266925    AY266925 Gadus mor
c  20   14.4       57.6      74     5   AY266926    AY266926 Gadus mor
c  21   14.4       57.6      74     5   AY266927    AY266927 Gadus mor
c  22   14.4       57.6      74     5   AY266930    AY266930 Gadus mor
c  23   14.4       57.6      74     5   AY266932    AY266932 Gadus mor
c  24   14.4       57.6      74     5   AY266939    AY266939 Gadus mor
c  25   14.4       57.6      74     5   AY266944    AY266944 Gadus mor
c  26   14.4       57.6      74     5   AY266949    AY266949 Gadus mor
c  27   14.4       57.6      74     5   AY266951    AY266951 Gadus mor
c  28   14.4       57.6      74     5   AY266952    AY266952 Gadus mor
c  29   14.4       57.6      74     5   AY266954    AY266954 Gadus mor
c  30   14.4       57.6      74     5   AY266956    AY266956 Gadus mor
c  31   14.4       57.6      74     5   AY266964    AY266964 Gadus mor
c  32   14.4       57.6      74     5   AY266966    AY266966 Gadus mor
c  33   14.4       57.6      74     5   AY266967    AY266967 Gadus mor
c  34   14.4       57.6      74     5   AY266968    AY266968 Gadus mor
c  35   14.4       57.6      74     5   AY266973    AY266973 Gadus mor
c  36   14.4       57.6      74     5   AY266974    AY266974 Gadus mor
c  37   14.4       57.6      74     5   AY266975    AY266975 Gadus mor
c  38   14.2       31         5     5   AY266980    AY266980 Gadus mor
c  39   14.2       56.8      49     6   BD002349    BD002349 Gene comp
c  40   14.2       56.8      49     6   AR032793    AR032793 Sequence
c  41   14.2       56.8      49     6   AR032793    AR032793 Sequence
c  42   14.2       56.8      49     6   I29533      I29533 Sequence 40
c  43   14.2       56.8      49     6   I91207      I91207 Sequence 40
c  44   14.2       56.8      49     6   I91207      I91207 Sequence 40
c  45   14.2       56.8      49     6   AR209457    AR209457 Sequence
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```
                                      ALIGNMENTS

RESULT 1
CQ004908/c
LOCUS        CQ004908             51 bp    DNA      linear    PAT 16-JAN-2004
DEFINITION   Sequence 3548 from Patent WO0147944.
ACCESSION    CQ004908
VERSION      CQ004908.1  GI:41011540
KEYWORDS
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1
  AUTHORS    Shimkets,R.A. and Leach,M.
  TITLE      Nucleic acids containing single nucleotide polymorphisms and
             methods of use thereof
  JOURNAL    Patent: WO 0147944-A 3548 05-JUL-2001;
             Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1..51
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Accession number cg44018111"
ORIGIN

Query Match      63.2%;  Score 15.8;  DB 6;  Length 51;
Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
Matches   17;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy          1 TATTAAGGGGCCTGGCCCC 19
              ||||  ||||||||||||||
Db         31 TTTTAGGGGCCTGGCCCC 13
```

```
RESULT 2
CQ006075/c
LOCUS        CQ006075             50 bp    DNA      linear    PAT 16-JAN-2004
DEFINITION   Sequence 4715 from Patent WO0147944.
ACCESSION    CQ006075
VERSION      CQ006075.1  GI:41012707
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```
KEYWORDS
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE    1 (bases 1 to )
  AUTHORS     Shinkets,R.A. and Leach,M.
  TITLE       Nucleic acids containing single nucleotide polymorphisms and
              methods of use thereof
  JOURNAL     Patent: WO 0147944-A 4715 05-JUL-2001;
              Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     misc_feature    25..26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg43256169"

ORIGIN

Qy           4 TAAGGGGGCCTGGCCCCCT 20
                |||||||||||||||||||
Db          44 TAAGGGGGCCTGGCCACT 28

RESULT 3
CQ006077/c
LOCUS       CQ006077         50 bp    DNA         linear    PAT 16-JAN-2004
DEFINITION  Sequence 4717 from Patent WO0147944.
ACCESSION   CQ006077
VERSION     CQ006077.1  GI:41012709
KEYWORDS
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1
  AUTHORS    Shinkets,R.A. and Leach,M.
  TITLE      Nucleic acids containing single nucleotide polymorphisms and
             methods of use thereof
  JOURNAL    Patent: WO 0147944-A 4717 05-JUL-2001;
             Curagen Corporation (US)
FEATURES            Location/Qualifiers
     source         1..50
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"
     misc_feature   25..26
                    /note="Nucleotide deleted between bases 25 and 26
                    Accession number cg43256169"

ORIGIN

Query Match       61.6%;  Score 15.4;  DB 6;  Length 50;
Best Local Similarity   94.1%;    Pred. No. 4.5e+03;
Matches 16;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy           4 TAAGGGGGCCTGGCCCCCT 20
                |||||||||||||||||||
Db          18 TAAGGGGGCCTGGCCACT 2

RESULT 4
AR012502/c
LOCUS       AR012502         70 bp    DNA         linear    PAT 04-DEC-1998
DEFINITION  Sequence 117 from patent US 5763566.
ACCESSION   AR012502
```

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VERSION     AR012502.1  GI:3970492
KEYWORDS
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 70)
  AUTHORS    Jensen,K.B., Chen,H., Morris,K.N., Stephens,A. and Gold,L.
  TITLE      Systematic evolution of ligands by exponential enrichment: tissue
             SELEX
  JOURNAL    Patent: US 5763566-A 117 09-JUN-1998;
FEATURES            Location/Qualifiers
     source         1..70
                    /organism="unknown"
                    /mol_type="unassigned DNA"

ORIGIN

Qy           2 ATTAAGGGGGCCTGGCCCCCTTAATA 25
                ||||||||||||||||||| | ||
Db          60 AATAAGCCGGCCTGGGAGCTTTAAACA 37

RESULT 5
AR020330/c
LOCUS       AR020330         70 bp    DNA         linear    PAT 05-DEC-1998
DEFINITION  Sequence 117 from patent US 5789157.
ACCESSION   AR020330
VERSION     AR020330.1  GI:3974945
KEYWORDS
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 70)
  AUTHORS    Jensen,K.B., Chen,H., Morris,K.N., Stephens,A. and Gold,L.
  TITLE      Systematic evolution of ligands by exponential enrichment: tissue
             selex
  JOURNAL    Patent: US 5789157-A 117 04-AUG-1998;
FEATURES            Location/Qualifiers
     source         1..70
                    /organism="unknown"
                    /mol_type="unassigned DNA"

ORIGIN

Query Match       57.6%;  Score 14.4;  DB 6;  Length 70;
Best Local Similarity   75.0%;    Pred. No. 1.6e+04;
Matches 18;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy           2 ATTAAGGGGGCCTGGCCCCCTTAATA 25
                ||||||||||||||||||| | ||
Db          60 AATAAGCCGGCCTGGGAGCTTTAAACA 37

RESULT 6
AR109351/c
LOCUS       AR109351         70 bp    DNA         linear    PAT 14-FEB-2001
DEFINITION  Sequence 117 from patent US 6114120.
ACCESSION   AR109351
VERSION     AR109351.1  GI:12825627
KEYWORDS
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 70)
  AUTHORS    Jensen,K.B., Chen,H., Morris,K.N., Stephens,A. and Gold,L.
  TITLE      Systematic evolution of ligands by exponential enrichment: tissue
             selex
  JOURNAL    Patent: US 6114120-A 117 05-SEP-2000;
FEATURES            Location/Qualifiers
     source         1..70
                    /organism="unknown"
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ORIGIN
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Qy    2 ATTAAGGGGCGCCTGGCCCCCTTAATA 25
        |||||||||||||||| ||| |||| |
Db   60 AATAAGCGGCGCCTGGAGCTTTAACA 37
```

RESULT 7
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LOCUS       I82676                   117 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 117 from patent US 5712375.
ACCESSION   I82676
VERSION     I82676.1  GI:3210973
KEYWORDS    Unknown.
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Jensen,K.B., Chen,H., Morris,K.N., Stephens,A. and Gold,L.
  TITLE     Systematic evolution of ligands by exponential enrichment: tissue
            selex
  JOURNAL   Patent: US 5712375-A 117 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1..70
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
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Query Match     57.6%;  Score 14.4;  DB 6;  Length 70;
Best Local Similarity 75.0%;  Pred. No.1.6e+04;
Matches 18;  Conservative   0;  Mismatches 6;  Indels   0;  Gaps   0;

Qy    2 ATTAAGGGGCGCCTGGCCCCCTTAATA 25
        |||||||||||||||| ||| |||| |
Db   60 AATAAGCGGCGCCTGGAGCTTTAACA 37
```

RESULT 8
```
LOCUS       AR368542                  70 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 117 from patent US 6376474.
ACCESSION   AR368542
VERSION     AR368542.1  GI:3460269
KEYWORDS    Unknown.
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Heilig,J.S. and Gold,L.
  TITLE     Systematic evolution of ligands by exponential enrichment: tissue
            SELEX
  JOURNAL   Patent: US 6376474-A 117 23-APR-2002;
            Gilead Sciences, Inc.; Foster City, CA
FEATURES             Location/Qualifiers
     source          1..70
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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```
Query Match     57.6%;  Score 14.4;  DB 6;  Length 70;
Best Local Similarity 75.0%;  Pred. No.1.6e+04;
Matches 18;  Conservative   0;  Mismatches 6;  Indels   0;  Gaps   0;

Qy    2 ATTAAGGGGCGCCTGGCCCCCTTAATA 25
        |||||||||||||||| ||| |||| |
Db   60 AATAAGCGGCGCCTGGAGCTTTAACA 37
```

RESULT 9
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LOCUS       AR391734                  70 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 117 from patent US 6613526.
ACCESSION   AR391734
VERSION     AR391734.1  GI:40115328
KEYWORDS    WOX;.
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Heilig,J.S. and Gold,L.
  TITLE     Systematic evolution of ligands by exponential enrichment: tissue
            selex
  JOURNAL   Patent: US 6613526-A 117 02-SEP-2003;
            Gilead Sciences, Inc.; Foster City, CA;
FEATURES             Location/Qualifiers
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Best Local Similarity 75.0%;  Pred. No.1.6e+04;
Matches 18;  Conservative   0;  Mismatches 6;  Indels   0;  Gaps   0;

Qy    2 ATTAAGGGGCGCCTGGCCCCCTTAATA 25
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RESULT 10
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LOCUS       AY266911                  74 bp    DNA     linear   VRT 16-DEC-2003
DEFINITION  Gadus morhua isolate TFA7.04 haplotype S02 mitochondrial
            tRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION   AY266911
VERSION     AY266911.1  GI:33089797
KEYWORDS    .
SOURCE      mitochondrion Gadus morhua (Atlantic cod)
  ORGANISM  Gadus morhua
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Extent of mitochondrial DNA sequence variation in Atlantic cod from
            the Faroe Islands: a resolution of gene genealogy
  JOURNAL   Heredity 91 (6), 557-564 (2003)
   PUBMED   14560303
REFERENCE   2  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2003) Institute of Biology, University of
            Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
FEATURES             Location/Qualifiers
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                     /organelle="mitochondrion"
                     /mol_type="genomic DNA"
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Best Local Similarity 75.0%;  Pred. No.1.6e+04;
Matches 18;  Conservative   0;  Mismatches 6;  Indels   0;  Gaps   0;

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Db   60 AATAAGCGGCGCCTGGAGCTTTAACA 37
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RESULT 11
AY266914/c
LOCUS       AY266914               74 bp    DNA     linear   VRT 16-DEC-2003
DEFINITION  Gadus morhua isolate TFA7.07 haplotype S06 mitochondrial
            tRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION   AY266914
VERSION     AY266914.1  GI:33089800
KEYWORDS    .
SOURCE      mitochondrion Gadus morhua (Atlantic cod)
  ORGANISM  Gadus morhua
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Extent of mitochondrial DNA sequence variation in Atlantic cod from
            the Faroe Islands: a resolution of gene genealogy
  JOURNAL   Heredity 91 (6), 557-564 (2003)
  PUBMED    14560303
REFERENCE   2  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2003) Institute of Biology, University of
            Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:8049"
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Db         33 ATTANGGGGGGGTCTCCCGGTAATA 10


RESULT 12
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LOCUS       AY266915               74 bp    DNA     linear   VRT 16-DEC-2003
DEFINITION  Gadus morhua isolate TFA7.08 haplotype S06 mitochondrial
            tRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION   AY266915
VERSION     AY266915.1  GI:33089801
KEYWORDS    .
SOURCE      mitochondrion Gadus morhua (Atlantic cod)
  ORGANISM  Gadus morhua
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Extent of mitochondrial DNA sequence variation in Atlantic cod from
            the Faroe Islands: a resolution of gene genealogy
  JOURNAL   Heredity 91 (6), 557-564 (2003)
  PUBMED    14560303
REFERENCE   2  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2003) Institute of Biology, University of
            Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
FEATURES             Location/Qualifiers
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                     /organelle="mitochondrion"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:8049"
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ORIGIN

Query Match             57.6%;  Score 14.4;  DB 5;  Length 74;
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  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 ATTAAGGGGGCCTGGCCCCTTAATA 25
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Db         33 ATTANGGGGGGGTCTCCCGGTAATA 10


RESULT 13
AY266916/c
LOCUS       AY266916               74 bp    DNA     linear   VRT 16-DEC-2003
DEFINITION  Gadus morhua isolate TFA7.09 haplotype S06 mitochondrial
            tRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION   AY266916
VERSION     AY266916.1  GI:33089802
KEYWORDS    .
SOURCE      mitochondrion Gadus morhua (Atlantic cod)
  ORGANISM  Gadus morhua
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Extent of mitochondrial DNA sequence variation in Atlantic cod from
            the Faroe Islands: a resolution of gene genealogy
  JOURNAL   Heredity 91 (6), 557-564 (2003)
  PUBMED    14560303
REFERENCE   2  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2003) Institute of Biology, University of
            Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
FEATURES             Location/Qualifiers
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                     /organelle="mitochondrion"
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                     /db_xref="taxon:8049"
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ORIGIN

Query Match             57.6%;  Score 14.4;  DB 5;  Length 74;
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  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Db         33 ATTATGGGGGGGTCTCCCGGTAATA 10
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RESULT 14

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LOCUS       AY266917/c                 74 bp    DNA     linear   VRT 16-DEC-2003
DEFINITION  Gadus morhua isolate TFA7.10 haplotype S03 mitochondrial
            tRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION   AY266917
VERSION     AY266917.1  GI:33089803
KEYWORDS    .
SOURCE      mitochondrion Gadus morhua (Atlantic cod)
  ORGANISM  Gadus morhua
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Extent of mitochondrial DNA sequence variation in Atlantic cod from
            the Faroe Islands: a resolution of gene genealogy
  JOURNAL   Heredity 91 (6), 557-564 (2003)
   PUBMED   14560303
REFERENCE   2  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2003) Institute of Biology, University of
            Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:8049"
                     /haplotype="S03"
                     /country="Faroe Islands"
     misc_feature    1..74
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ORIGIN

Query Match             57.6%;  Score 14.4;  DB 5;  Length 74;
Best Local Similarity   75.0%;  Pred. No. 1.6e+04;
Matches   18;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy          2 ATTAAGGGGCCTGGCCCCCTTAATA 25
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Db         33 ATTATGGGGGCGTCCCCGGGTAATA 10
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RESULT 15

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DEFINITION  Gadus morhua isolate TFA7.11 haplotype S06 mitochondrial
            tRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION   AY266918
VERSION     AY266918.1  GI:33089804
KEYWORDS    .
SOURCE      mitochondrion Gadus morhua (Atlantic cod)
  ORGANISM  Gadus morhua
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Extent of mitochondrial DNA sequence variation in Atlantic cod from
            the Faroe Islands: a resolution of gene genealogy
  JOURNAL   Heredity 91 (6), 557-564 (2003)
   PUBMED   14560303
REFERENCE   2  (bases 1 to 74)
  AUTHORS   Sigurgislason,H. and Arnason,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2003) Institute of Biology, University of
            Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
FEATURES             Location/Qualifiers
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                     /organelle="mitochondrion"
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                     /db_xref="taxon:8049"
                     /haplotype="S06"
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     misc_feature    1..74
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ORIGIN

Query Match             57.6%;  Score 14.4;  DB 5;  Length 74;
Best Local Similarity   75.0%;  Pred. No. 1.6e+04;
Matches   18;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy          2 ATTAAGGGGCCTGGCCCCCTTAATA 25
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Job time : 1993 secs
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OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2006 Bioacceleration Ltd.   GenCore version 5.1.7

Run on: February 7, 2006, 12:06:52 ; Search time 794 Seconds
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Title: US-10-613-390B-1
Perfect score: 25
Sequence: 1 tattaagggcctggcccctaata 25

Scoring table: IDENTITY_NUC
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	ID	Description
1	25	100.0	25	7	US-10-613-390B-1	Sequence 1, Appli
c 2	23.4	93.6	25	7	US-10-613-390B-1	Sequence 1, Appli
c 3	17.4	69.6	25	9	US-10-809-189-116728	Sequence 116728,
c 4	15.8	63.2	25	9	US-10-719-900-27015	Sequence 27015, A
c 5	15.8	63.2	25	8	US-10-719-900-27016	Sequence 27016, A
c 6	15.8	63.2	25	9	US-10-809-189-116728	Sequence 116728, A
7	15.8	63.2	25	10	US-10-809-189-116728	Sequence 189638,
c 8	15.8	63.2	25	10	US-11-036-317-226389	Sequence 226389,
c 9	15.8	63.2	25	10	US-11-036-317-273256	Sequence 273256,
c 10	15.8	63.2	25	10	US-11-036-317-295882	Sequence 295882,
c 11	15.8	63.2	25	10	US-11-036-317-303549	Sequence 303549,
c 12	15.8	63.2	25	10	US-11-036-317-374272	Sequence 374272,
c 13	15.8	63.2	25	10	US-11-036-317-739211	Sequence 739211,
c 14	15.4	61.6	25	10	US-11-060-756-172272	Sequence 172272,
c 15	15.2	60.8	25	7	US-10-719-956-370902	Sequence 370902,
c 16	15.2	60.8	25	7	US-10-719-956-134872	Sequence 134872,
c 17	14.8	59.2	25	9	US-10-809-189-86335	Sequence 86335, A
c 18	14.8	59.2	25	9	US-10-809-189-86336	Sequence 86336, A
c 19	14.8	59.2	25	10	US-11-036-317-451864	Sequence 451864,
c 20	14.6	58.4	25	7	US-10-719-956-567778	Sequence 567778,
c 21	14.4	57.6	25	7	US-10-719-956-567779	Sequence 567779,
c 22	14.4	57.6	25	10	US-11-036-317-208481	Sequence 208481,
c 23	14.4	57.6	25	10	US-11-036-317-249444	Sequence 249444,
c 24	14.4	57.6	25	10	US-11-036-317-263488	Sequence 263488,
c 25	14.4	57.6	25	10	US-11-036-317-298920	Sequence 298920,
c 26	14.4	57.6	25	10	US-11-036-317-343406	Sequence 343406,
c 27	14.4	57.6	25	10	US-11-036-317-361767	Sequence 361767,
c 28	14.4	57.6	25	10	US-11-060-756-134392	Sequence 134392,
c 29	14.4	57.6	25	10	US-11-060-756-297112	Sequence 297112,
c 30	14.4	70	25	5	US-10-077-319-117	Sequence 117, App
c 31	14.2	56.8	25	7	US-10-719-956-305034	Sequence 305034,
c 32	14.2	56.8	25	8	US-10-719-900-27015	Sequence 27015, A
c 33	14.2	56.8	25	9	US-10-719-900-27015	Sequence 27015, A
c 34	14.2	56.8	25	8	US-10-719-900-27016	Sequence 27016, A
c 35	14.2	56.8	25	9	US-11-060-756-255528	Sequence 255528,
c 36	14.2	56.8	25	8	US-10-809-189-800772	Sequence 800772,
c 37	14.2	56.8	25	9	US-10-809-189-26177	Sequence 26177, A
c 38	14.2	56.8	25	9	US-10-956-157-227800	Sequence 227800,
c 39	14.2	56.8	25	8	US-11-036-317-189638	Sequence 189638,
c 40	14.2	56.8	25	8	US-11-036-317-226389	Sequence 226389,
c 41	14.2	56.8	25	8	US-11-036-317-273256	Sequence 273256,
c 42	14.2	56.8	25	8	US-11-036-317-295882	Sequence 295882,
c 43	14.2	56.8	25	10	US-11-036-317-303549	Sequence 303549,
c 44	14.2	56.8	25	10	US-11-036-317-374272	Sequence 374272,
c 45	14.2	56.8	25	10	US-11-036-317-739212	Sequence 739212,

ALIGNMENTS

RESULT 1
US-10-613-390B-1
; Sequence 1, Application US/10613390B
; Publication No. US2004012744201
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning Inc
; TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders
; FILE REFERENCE: 60/400,137
; CURRENT APPLICATION NUMBER: US/10/613,390B
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10/613390
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic primer
US-10-613-390B-1

Query Match   100.0%; Score 25; DB 7; Length 25;
Best Local Similarity   100.0%;
Matches   25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 TATTAAGGGCCTGGCCCCTAATA 25
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Db   1 TATTAAGGGCCTGGCCCCTAATA 25

RESULT 2
US-10-613-390B-1/c
; Sequence 1, Application US/10613390B
; Publication No. US2004012744201
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning Inc
; TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders
; FILE REFERENCE: 60/400,137
; CURRENT APPLICATION NUMBER: US/10/613,390B
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/10/613390
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1

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;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic primer
US-10-613-390B-1

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Best Local Similarity   96.0%;  Pred. No. 0.3;
Matches  24;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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RESULT 3
US-10-809-189-116728/c
Sequence 116728, Application US/10809189
Publication No. US20050048531A1
GENERAL INFORMATION:
;   APPLICANT: Michael Mittmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/10/809,189
;   CURRENT FILING DATE: 2004-03-25
;   PRIOR APPLICATION NUMBER: US/09/396,196
;   PRIOR FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 116728
;     LENGTH: 25
;     TYPE: DNA
;     ORGANISM: mus musculus
US-10-809-189-116728

Query Match             69.6%;  Score 17.4;  DB 9;  Length 25;
Best Local Similarity   94.7%;  Pred. No. 2.3e+02;
Matches  18;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    6 AGGGGGCCTGCCCCCTTAAT 24
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Db   25 AGGGGCCTGGCACCTTAAT 7
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RESULT 4
US-10-719-900-27015/c
Sequence 27015, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
;   APPLICANT: Xue Mei Zhou
;   TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;   FILE REFERENCE: 3528.1
;   CURRENT APPLICATION NUMBER: US/10/719,900
;   CURRENT FILING DATE: 2003-11-20
;   PRIOR APPLICATION NUMBER: 60/427,808
;   PRIOR FILING DATE: 2002 11 20
;   NUMBER OF SEQ ID NOS: 982914
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;   SEQ ID NO 27015
;     LENGTH: 25
;     TYPE: DNA
;     ORGANISM: Mus musculus
US-10-719-900-27015

Query Match             63.2%;  Score 15.8;  DB 8;  Length 25;
Best Local Similarity   89.5%;  Pred. No. 1.4e+03;
Matches  17;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;
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Qy    6 AGGGGGCCTGGCCCCCTTAAT 24
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Db   24 AGGGACCTGGCTGCCTTAAT 6
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```
RESULT 5
US-10-719-900-27016/c
Sequence 27016, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
;   APPLICANT: Xue Mei Zhou
;   TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;   FILE REFERENCE: 3528.1
;   CURRENT APPLICATION NUMBER: US/10/719,900
;   CURRENT FILING DATE: 2003-11-20
;   PRIOR APPLICATION NUMBER: 60/427,808
;   PRIOR FILING DATE: 2002 11 20
;   NUMBER OF SEQ ID NOS: 982914
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;   SEQ ID NO 27016
;     LENGTH: 25
;     TYPE: DNA
;     ORGANISM: Mus musculus
US-10-719-900-27016

Query Match             63.2%;  Score 15.8;  DB 8;  Length 25;
Best Local Similarity   89.5%;  Pred. No. 1.4e+03;
Matches  17;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;
```

```
Qy    6 AGGGGGCCTGGCCCCCTTAAT 24
        |||||||||||| |||||||
Db   24 AGGGACCTGGCTGCCTTAAT 6
```

```
RESULT 6
US-10-809-189-116728
Sequence 116728, Application US/10809189
Publication No. US20050048531A1
GENERAL INFORMATION:
;   APPLICANT: Michael Mittmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/10/809,189
;   CURRENT FILING DATE: 2004-03-25
;   PRIOR APPLICATION NUMBER: US/09/396,196
;   PRIOR FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 116728
;     LENGTH: 25
;     TYPE: DNA
;     ORGANISM: mus musculus
US-10-809-189-116728

Query Match             63.2%;  Score 15.8;  DB 9;  Length 25;
Best Local Similarity   89.5%;  Pred. No. 1.4e+03;
Matches  17;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;
```

```
Qy    2 ATTAAGGGGGCCTGCCCCCT 20
        ||||||||||| |||||||||
Db    7 ATTAAGGTGCCAGGCCCCT 25
```

```
RESULT 7
US-11-036-317-189638
Sequence 189638, Application US/11036317
Publication No. US20050214823A1
```

; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 189638
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-189638

Qy   6 AGGGGGCCTGGCCCCTTAAT 24
            ||| ||||||||||||||
Db   3 AGGAGCCTGGCCCCTTCAT 21

RESULT 8
US-11-036-317-226389
; Sequence 226389, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 226389
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-226389

Query Match   63.2%;   Score 15.8; DB 10;   Length 25;
Best Local Similarity   89.5%;   Pred. No. 1.4e+03;
Matches 17; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   6 AGGGGGCCTGGCCCCTTAAT 24
            ||| ||||||||||||||
Db   4 AGGAGCCTGGCCCCTTCAT 22

RESULT 9
US-11-036-317-273256
; Sequence 273256, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 273256
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-273256

Query Match   63.2%;   Score 15.8; DB 10;   Length 25;
Best Local Similarity   89.5%;   Pred. No. 1.4e+03;
Matches 17; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   6 AGGGGGCCTGGCCCCTTAAT 24
            ||| ||||||||||||||
Db   5 AGGAGCCTGGCCCCTTCAT 23

RESULT 10
US-11-036-317-295882
; Sequence 295882, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 295882
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-295882

Query Match   63.2%;   Score 15.8; DB 10;   Length 25;
Best Local Similarity   89.5%;   Pred. No. 1.4e+03;
Matches 17; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   6 AGGGGGCCTGGCCCCTTAAT 24
            ||| ||||||||||||||
Db   7 AGGAGCCTGGCCCCTTCAT 25

RESULT 11
US-11-036-317-303549
; Sequence 303549, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 303549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-303549

Query Match   63.2%;   Score 15.8; DB 10;   Length 25;
Best Local Similarity   89.5%;   Pred. No. 1.4e+03;
Matches 17; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   6 AGGGGGCCTGGCCCCTTAAT 24
            ||| ||||||||||||||
Db   2 AGGAGCCTGGCCCCTTCAT 20

RESULT 12
US-11-036-317-374272
; Sequence 374272, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;   APPLICANT: Williams, Alan
;   APPLICANT: Blume, John
;   TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;   FILE REFERENCE: 3654.1
;   CURRENT APPLICATION NUMBER: US/11/036,317
;   CURRENT FILING DATE: 2005-01-13
;   PRIOR APPLICATION NUMBER: US 60/536,639
;   PRIOR FILING DATE: 2004-01-13
;   NUMBER OF SEQ ID NOS: 991174
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 374272
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-374272

Query Match   63.2%; Score 15.8; DB 10; Length 25;
Best Local Similarity   89.5%; Pred. No. 1.4e+03;
Matches   17; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   6 AGGGGCCTGGCCCCTTAAT 24
              |||||||||||||| ||||
Db   6 AGGAGCCTGGCCCCTTCAT 24

RESULT 13
US-11-036-317-739211/c
; Sequence 739211, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;   APPLICANT: Williams, Alan
;   APPLICANT: Blume, John
;   TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;   FILE REFERENCE: 3654.1
;   CURRENT APPLICATION NUMBER: US/11/036,317
;   CURRENT FILING DATE: 2005-01-13
;   PRIOR APPLICATION NUMBER: US 60/536,639
;   PRIOR FILING DATE: 2004-01-13
;   NUMBER OF SEQ ID NOS: 991174
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 739211
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-739211

Query Match   61.6%; Score 15.4; DB 10; Length 25;
Best Local Similarity   94.1%; Pred. No. 2.1e+03;
Matches   16; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   6 AGGGGCCTGGCCCCTTA 22
              |||||||||||| ||||
Db   25 AGGGGGCCTGGCCCCATA 9

RESULT 14
US-11-060-756-172272/c
; Sequence 172272, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;   APPLICANT: Wyeth
;   APPLICANT: Mounts, William Martin
;   TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;   TITLE OF INVENTION: Target Genes
;   FILE REFERENCE: AM101083 (031896-042000)
;   CURRENT APPLICATION NUMBER: US/11/060,756
;   CURRENT FILING DATE: 2005-02-18
;   NUMBER OF SEQ ID NOS: 303284

RESULT 15
US-10-719-956-370902
; Sequence 370902, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;   APPLICANT: Xue Mei Zhou
;   TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;   FILE REFERENCE: 3527.1
;   CURRENT APPLICATION NUMBER: US/10/719,956
;   CURRENT FILING DATE: 2003-11-20
;   PRIOR APPLICATION NUMBER: 60/427,836
;   PRIOR FILING DATE: 2002 11 20
;   NUMBER OF SEQ ID NOS: 699466
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 370902
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-370902

Query Match   60.8%; Score 15.2; DB 7; Length 25;
Best Local Similarity   85.0%; Pred. No. 2.7e+03;
Matches   17; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   3 TTAAGGGGCCTGGCCCCTTA 22
              |||||||| |||||||
Db   4 TAATGTGGCCTGGCCCCTTA 23

Search completed: February 7, 2006, 12:22:29
Job time : 795 secs

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.7

Run on: February 7, 2006, 11:01:48 ; Search time 3599 Seconds (without alignments) 325.001 Million cell updates/sec

Title: US-10-613-390B-1
Perfect score: 25
Sequence: 1 tattaaggggcctggcccttaata 25
Scoring table: IDENTITY_NUC
Scoring table: Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 2339541228 residues
Total number of hits satisfying chosen parameters: 778150
Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Match Length	DB	ID	Description
1		16	64.0	83	5	BU812825	N001H03 P
2		15.8	63.2	78	1	AW250424	2822310.3
3	c	15.4	61.6	40	9	AZ371110	1M012210S
4	c	15.4	61.6	40	9	AZ371110	1M012210S
5	c	15.4	61.6	83	9	AZ440331	1M0231A20
6	c	15.2	60.8	98	1	AW770417	h181a12.x
7		15	60.0	64	1	AI149654	qf37c02.x
8	c	15	60.0	70	10	CG527767	OST106096
9	c	15	60.0	73	1	AW251001	2821159.3
10	c	15	60.0	86	10	CG524805	OST99167
11	c	15	60.0	94	7	CK428180	lajllg07.
12	c	14.6	58.4	53	10	CL880134	abf42c10.
13		14.6	58.4	61	11	CR169973	Forward s
14		14.6	58.4	64	10	CG650062	OST406254
15	c	14.6	58.4	64	10	CG650062	OST406254
16	c	14.4	57.6	42	10	BX650299	Arabidops
17	c	14.4	57.6	83	5	BU812825	N001H03 P
18	c	14.4	57.6	84	6	CF102969	hac40a08.
19	c	14.4	57.6	91	6	CF641086	D35 D11 F
20	c	14.2	56.8	46	10	CL529021	HIV62B10.
21	c	14.2	56.8	57	10	AZ651810	AZ651810
22	c	14.2	56.8	66	10	CG482226	OST15124
23	c	14.2	56.8	78	1	AW250424	2822310.3
24	c	14.2	56.8	84	10	CZ444284	AB0876 Sa
25	c	14.2	56.8	89	6	CB930280	ri93a05.y
26	c	14.2	56.8	89	6	CB930280	ri93a05.y
27	c	14	56.0	28	1	AA870545	vg23a04.r
28		14	56.0	55	11	GGA350127	Gallus ga
29	c	13.8	55.2	46	11	AJ232133	Gallus ga
30	c	13.8	55.2	58	10	AI582875	ts07a07.x
31	c	13.8	55.2	70	9	AJ587174	Arabidops
32	c	13.8	55.2	71	10	AZ484117	1M031ON16
33		13.8	55.2	71	10	CW083263	104_425_1
34	c	13.8	55.2	78	10	CW083263	89M06.40
35	c	13.8	55.2	79	1	AI686688	tu35g10.x
36		13.8	55.2	83	9	AZ440331	1M0231A20
37		13.8	55.2	85	11	CR102161	Reverse s
38		13.8	55.2	96	3	BJ076360	BJ076360
39		13.8	55.2	96	11	CR131012	Reverse s
40		13.8	55.2	97	10	CD979428	OAG3b11.y
41	c	13.8	55.2	100	10	CG553173	OST165393
42	c	13.6	54.4	9	10	AZ423820	1M0203P22
43	c	13.6	54.4	67	10	CG525840	OST101409
44	c	13.6	54.4	71	10	AA452589	zx39f02.s
45		13.6	54.4	76	10	CG573029	OST204293

ALIGNMENTS

RESULT 1
BU812825

LOCUS   BU812825   83 bp   mRNA   linear   EST 15-OCT-2002
DEFINITION N001H03 Populus bark cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION   BU812825
VERSION   BU812825.1 GI:23968143
KEYWORDS   EST.
SOURCE   Populus tremula x Populus tremuloides
ORGANISM   Populus tremula x Populus tremuloides
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE   1 (bases 1 to 83)
AUTHORS   Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
TITLE   The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
JOURNAL   Unpublished (2002)
COMMENT   Contact: BHALERAO RUPALI R.
            Umea Plant Science Center
            Department of Plant Physiology
            University of Umea, 901 87 Umea, Sweden
            Tel: +46 90 786 5279
            Fax: +46 90 786 6676
            Email: rupali.bhalerao@plantphys.umu.se.
FEATURES   Location/Qualifiers
     source 1..83
             /organism="Populus tremula x Populus tremuloides"
             /mol_type="mRNA"
             /db_xref="taxon:47664"
             /tissue_type="bark"
             /clone_lib="Populus bark cDNA library"
ORIGIN

Query Match 64.0%; Score 16; DB 5; Length 83;
Best Local Similarity 79.2%;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATTAAGGGGCCTGGCCCCTTAATA 25
        ||||| ||| || |||||||||
Db 33 ATTAAAGGGACTGGTTACTTAATA 56

RESULT 2
AW250424

LOCUS   AW250424   78 bp   mRNA   linear   EST 07-JAN-2000
DEFINITION 2822310.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822310 3',
            mRNA sequence.
ACCESSION   AW250424
VERSION   AW250424.1 GI:6593417
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 78)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Other_ESTs: 2822310.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DFP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 22
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 78 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM9 row: B column: 7
            High quality sequence stop: 22.
FEATURES   Location/Qualifiers
     source   1..78
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822310"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Query Match   63.2%; Score 15.8; DB 1; Length 78;
  Best Local Similarity   89.5%;
  Matches   17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   5 AAGGGGGCCTGGGCCCCTTAA 23
              ||||||||||||| ||||||
Db   15 AAAGGGGCCTGGGTCCCTTAA 33

RESULT 3
LOCUS   AZ371110   40 bp   DNA   linear   GSS 02-OCT-2000
DEFINITION 1M0122I05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0122I05 F, genomic survey sequence.
ACCESSION   AZ371110
VERSION   AZ371110.1 GI:10484810

KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 40)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert length: 10000 Std Error: 0.00
            Insert length: 10000
            Plate: 0122 row: I column: 05
            Seq primer: CGTTCGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 40.
FEATURES   Location/Qualifiers
     source   1..40
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0122I05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F- "
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: pWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|473214|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid RI. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

Query Match   61.6%; Score 15.4; DB 9; Length 40;
  Best Local Similarity   76.0%;
  Matches   19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy   1 TATTAAGGGGCCTGGCCCCTTAATA 25
              |||| ||| ||||||| ||||||
Db   13 TATTATGGGTTATGGGCCCATTAATA 37

RESULT 4
LOCUS   AZ371110/c   40 bp   DNA   linear   GSS 02-OCT-2000
DEFINITION 1M0122I05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0122I05 F, genomic survey sequence.
ACCESSION   AZ371110

```
VERSION     AZ371110.1  GI:10484810
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0122   row: I   column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1..40
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0122I05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN


RESULT 5
LOCUS        AZ440331        83 bp        DNA        linear        GSS 03-OCT-2000
DEFINITION   1M0231A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
             clone UUGC1M0231A20 F, genomic survey sequence.

Query Match           61.6%;   Score 15.4;   DB 9;   Length 40;
Best Local Similarity 76.0%;   Pred. No. 2.3e+04;
Matches 19;   Conservative 0;   Mismatches 6;   Indels 0;   Gaps 0;

Qy  1 TATTAAGGGGGCCTGGGCCCCTTAATA 25
       |||||| |||||| ||||| ||||
Db 37 TATTAATGGGCCCCATACCCATAATA 13
```

```
ACCESSION   AZ440331
VERSION     AZ440331.1  GI:10564344
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 83)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0231   row: A   column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 83.
FEATURES             Location/Qualifiers
     source          1..83
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0231A20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN


RESULT 6
LOCUS        AW770417        98 bp        mRNA        linear        EST 04-MAY-2000
DEFINITION   h181a12.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3007582 3',

Query Match           61.6%;   Score 15.4;   DB 9;   Length 83;
Best Local Similarity 94.1%;   Pred. No. 2.4e+04;
Matches 16;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  8 GGGGCCTGGCCCCTTAAT 24
       |||||| |||||||||||
Db 68 GGGGCCTTGCCCCTTAAT 52
```

mRNA sequence.

```
ACCESSION   AW770417
VERSION     AW770417.1  GI:7702459
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 98)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Chris Moskaluk, M.D., Ph.D; Michael R.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 73.
FEATURES             Location/Qualifiers
     source          1..98
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3007582"
                     /tissue_type="2 pooled Wilms' tumors, one primary and one
                     metastatic to brain"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid13"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Library constructed by Life Technologies."
ORIGIN
```

```
RESULT 7
LOCUS       AI149654                64 bp    mRNA    linear    EST 10-NOV-1998
DEFINITION  qf37c02.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1752194
            3' similar to gb:M61866 ZINC FINGER PROTEIN 85 (HUMAN);, mRNA
            sequence.
ACCESSION   AI149654
VERSION     AI149654.1  GI:3678123
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
```

```
Query Match             60.8%;  Score 15.2;  DB 1;  Length 98;
Best Local Similarity   85.0%;  Pred. No. 3.1e+04;
Matches     17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 AGGGGGCCTGGGCCCCCTTAATA 25
              |||||||||||||||||||| ||
Db         95 AGGGGGCCTGGGCCCCCAGAACA 76
```

```
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1082  Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..64
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1752194"
                     /sex="male"
                     /lab_host="DH10B"
                     /clone_lib="Soares testis NHT"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGACGCGGCGCGCCAATTTTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
```

```
RESULT 8
LOCUS       CG527767                70 bp    mRNA    linear    GSS 01-OCT-2003
DEFINITION  OST106096 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST106096,
            mRNA sequence.
ACCESSION   CG527767
VERSION     CG527767.1  GI:37314339
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
   PUBMED   14610273
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: material@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
```

```
Query Match             60.0%;  Score 15;  DB 1;  Length 64;
Best Local Similarity   78.3%;  Pred. No. 3.7e+04;
Matches     18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TATTAAGGGGCCTGGCCCCCTTAA 23
              |||||| ||||||||| ||| |||
Db         12 TATAAGGGGTCTTCGGCGTCTTAA 34
```

```
     source          1..70
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST106096"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"

Qy
Query Match    60.0%;  Score 15;  DB 10;  Length 70;
Best Local Similarity  78.3%;  Pred. No. 3.7e+04;
Matches 18;  Conservative 0;  Mismatches 5;  Indels 0;  Gaps 0;

Qy   2 ATTAAGGGGCCTGGCCCCTTAAT 24
         ||| ||| |||||| ||| |||
Db  53 ATCATGGGGTCCTGGCTCCTGAAT 31


RESULT 9
AW251001/c
LOCUS       AW251001                73 bp    mRNA    linear    EST 07-JAN-2000
DEFINITION  2821159.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821159 3',
            mRNA sequence.
ACCESSION   AW251001
VERSION     AW251001.1  GI:6591947
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 73)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other ESTs: 2821159.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 73 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM6    row: B  column: 8
            High quality sequence stop: 10.
FEATURES             Location/Qualifiers
     source          1..73
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821159"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
```

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ORIGIN
                    the laboratory of Gerald M. Rubin (University of
                    California, Berkeley) using ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies)."


RESULT 10
CG524805/c
LOCUS       CG524805                86 bp    mRNA    linear    GSS 01-OCT-2003
DEFINITION  OST99167 Mus musculus cDNA clone OST99167,
            mRNA sequence.
ACCESSION   CG524805
VERSION     CG524805.1  GI:37311377
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 86)
AUTHORS     Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
TITLE       Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
PUBMED      14610273
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1..86
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST99167"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

Qy
Query Match    60.0%;  Score 15;  DB 1;  Length 73;
Best Local Similarity  78.3%;  Pred. No. 3.7e+04;
Matches 18;  Conservative 0;  Mismatches 5;  Indels 0;  Gaps 0;

Qy   3 TTAAGGGGCCTGGCCCCTTAATA 25
         |||||| || |||||| || |||
Db  52 TTCCGGGGGGGGTCGGCCCCTCAATA 30


RESULT 11
CK428180/c
LOCUS       CK428180                94 bp    mRNA    linear    EST 06-JAN-2004
DEFINITION  lajl1g07.y1 Gastric Epithelial Progenitor 2 Mus musculus cDNA 5',
            mRNA sequence.
ACCESSION   CK428180

Qy
Query Match    60.0%;  Score 15;  DB 10;  Length 86;
Best Local Similarity  78.3%;  Pred. No. 3.8e+04;
Matches 18;  Conservative 0;  Mismatches 5;  Indels 0;  Gaps 0;

Qy   1 TATTAAGGGGCCTGGCCCCTTAA 23
         |||| ||||||||| |||||||
Db  84 TATTCCAGGGGTCGGCCCCTTGA 62
```

VERSION   CK428180.1 GI:40672576
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 94)
  AUTHORS   Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,
            Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,
            Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,
            Waterston,R. and Wilson,R.
  TITLE   WashU Stem cell EST Project
  JOURNAL   Unpublished (2002)
COMMENT   Contact: Jeff Gordon and Mike Lovett
            Washington University School of Medicine
            WashU, Human Genetics Division
            1st strand of cDNA was synthesized with reverse transcriptase and
            oligo(dT) beads, then cDNA was amplified by PCR using modified
            SMART primers. The final cDNA was cloned in pAMP1 vector in
            annealing reaction with Uracil DNA Glycosylase (UDG). Library
            constructed by Y.Korshunova and M. Lovett. Library materials
            provided by Mills JC & Gordon JI.
            Putative full length read
            Seq primer: -40RP from Gibco.
FEATURES   Location/Qualifiers
     source   1..94
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /tissue_type="Laser-captured isthmal cells from tox176
                     transgenic mice"
                     /dev_stage="adult"
                     /lab_host="DH5alpha"
                     /clone_lib="Gastric Epithelial Progenitor 2"
                     /note="Vector: pAMP1; 1st strand of cDNA was synthesized
                     with reverse transcriptase and oligo(dT) beads, then cDNA
                     was amplified by PCR using modified SMART primers. The
                     final cDNA was cloned in pAMP1 vector in annealing
                     reaction with Uracil DNA Glycosylase (UDG). Library
                     constructed by Y.Korshunova and M. Lovett. Library
                     materials provided by Mills JC & Gordon JI."
ORIGIN

Query Match   60.0%; Score 15; DB 7; Length 94;
  Best Local Similarity   78.3%;
  Matches   18; Conservative   0; Pred. No. 3.8e+04; Mismatches   5; Indels   0; Gaps   0;

Qy   1 TATTAAGGGGCCTGGCCCCTTAA 23
              ||||| |||||||||||| ||||
Db   43 TATTCTTGGGGCTGGCCCCTTTA 21

RESULT 12
CL880134/c
LOCUS   CL880134   53 bp   DNA   linear   GSS 30-AUG-2004
DEFINITION abf42c10.y1 Soybean random, unfiltered genomic library Glycine max
            genomic, genomic survey sequence.
ACCESSION   CL880134
VERSION   CL880134.1 GI:51614669
KEYWORDS   GSS.
SOURCE   Glycine max (soybean)
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 53)
  AUTHORS   Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,
            Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and
            Stacey,G.
  TITLE   Methylation filtered genomic sequences from Glycine max

JOURNAL   Unpublished (2004)
COMMENT   Contact: Gary Stacey
            University of Missouri
            108 Waters Hall, Columbia, MO 65211, USA
            Tel: 573-884-1267
            Fax: 573-882-0588
            Email: staceyg@missouri.edu
            LibID: 230
            Class: shotgun.
FEATURES   Location/Qualifiers
     source   1..53
                     /organism="Glycine max"
                     /mol_type="genomic DNA"
                     /cultivar="Williams 82"
                     /db_xref="taxon:3847"
                     /clone_lib="Soybean random, unfiltered genomic library"
                     /note="Vector: pOT2; Site 1; BstXI; Randomly sheared
                     genomic DNA ranging from 0.7-1.5 kb were end repaired and
                     ligated to BstXI linkers prior to cloning in BstXI-cut
                     pOT2. LibID: 230"
ORIGIN

Query Match   58.4%; Score 14.6; DB 10; Length 53;
  Best Local Similarity   81.0%; Pred. No. 5.6e+04;
  Matches   17; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 TATTAAGGGGCCTGGCCCCTT 21
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Db   38 TCTTAAGGTGGTTGGGCCCTT 18

RESULT 13
CR169973
LOCUS   CR169973   61 bp   DNA   linear   GSS 06-JUL-2004
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and
            chromosome engineering clone MHPN50C03, genomic survey sequence.
ACCESSION   CR169973
VERSION   CR169973.1 GI:49948822
KEYWORDS   GSS; genome survey sequence; MICER.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 61)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE   Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES   Location/Qualifiers
     source   1..61
                     /organism="Mus musculus"
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                     /db_xref="taxon:10090"
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ORIGIN

Query Match   58.4%; Score 14.6; DB 11; Length 61;
  Best Local Similarity   81.0%; Pred. No. 5.7e+04;
  Matches   17; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   2 ATTAAGGGGCCTGGCCCCTTA 22
              |||| ||||||||||||| |||
Db   16 ATTTACGAGCCTGGCCTCTTA 36

RESULT 14
CG650062
LOCUS   CG650062   64 bp   mRNA   linear   GSS 02-OCT-2003

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RESULT 15
LOCUS       CG650062/c
DEFINITION  OST406254 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST406254,
            mRNA sequence.
ACCESSION   CG650062
VERSION     CG650062.1  GI:37473911
KEYWORDS    GSS.
SOURCE      Mus musculus
ORGANISM    Mus musculus (house mouse)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 64)
AUTHORS     Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
TITLE       Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
PUBMED      14610273
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
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                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST406254"
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                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

Query Match     58.4%;  Score 14.6;  DB 10;  Length 64;
Best Local Similarity     70.8%;  Pred. No. 5.7e+04;
Matches  17;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy    1 TATTAAGGGGCCTCGGCCCCTTAAT 24
         ||| ||||| |||||| |||||| |||
Db   28 TTTTTNGGGGACNGGCCCCNAAAAT 51
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LOCUS       CG650062             64 bp    mRNA      linear    GSS 02-OCT-2003
DEFINITION  OST406254 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST406254,
            mRNA sequence.
ACCESSION   CG650062
VERSION     CG650062.1  GI:37473911
KEYWORDS    GSS.
SOURCE      Mus musculus
ORGANISM    Mus musculus (house mouse)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 64)
AUTHORS     Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
TITLE       Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
PUBMED      14610273
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1..64
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST406254"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

Query Match     58.4%;  Score 14.6;  DB 10;  Length 64;
Best Local Similarity     70.8%;  Pred. No. 5.7e+04;
Matches  17;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy    2 ATTTAAGGGGCCTGGCCCCCTTAATA 25
         ||| ||||||||| |||| |||| |||
Db   51 ATTTNGGGGCCNGTCCCCNAAAAA 28

Search completed: February 7, 2006, 12:06:36
Job time : 3603 secs
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OM nucleic - nucleic search, using sw model

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Run on: February 7, 2006, 11:27:28 ; Search time 163 Seconds
(without alignments)
287.171 Million cell updates/sec

Title: US-10-613-390B-1
Perfect score: 25
Sequence: 1 tattaagggcctggcccttaata 25
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3449518 seqs, 936177250 residues.
Total number of hits satisfying chosen parameters: 5005474
Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Pending_Patents_NA_New:*

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9: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
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12: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	15.6	62.4	60	11	US-11-130-645B-528520	Sequence 528520,
2	15.6	62.4	63	11	US-11-130-645B-150318	Sequence 150318,
3	15.6	62.4	64	11	US-11-130-645B-119663	Sequence 119663,
4	15.6	62.4	64	11	US-11-130-645B-139002	Sequence 139002,
5	15.6	62.4	64	11	US-11-130-645B-178751	Sequence 178751,
6	15.6	62.4	64	11	US-11-130-645B-236152	Sequence 236152,
7	15.6	62.4	64	11	US-11-130-645B-307585	Sequence 307585,
8	15.6	62.4	64	11	US-11-130-645B-333006	Sequence 333006,
9	15.6	62.4	64	11	US-11-130-645B-627039	Sequence 627039,
10	15.6	62.4	64	11	US-11-130-645B-688578	Sequence 688578,
11	15.4	61.6	64	11	US-11-130-645B-115601	Sequence 115601,
12	15.4	61.6	64	11	US-11-130-645B-235099	Sequence 235099,
13	15.4	61.6	64	11	US-11-130-645B-378454	Sequence 378454,
14	15.4	61.6	64	11	US-11-130-645B-378526	Sequence 378526,
15	15.4	61.6	64	11	US-11-130-645B-427234	Sequence 427234,
16	15.4	61.6	64	11	US-11-130-645B-459220	Sequence 459220,
17	15.4	61.6	64	11	US-11-130-645B-467734	Sequence 467734,
18	15.4	61.6	64	11	US-11-130-645B-569003	Sequence 569003,
19	15.2	60.8	63	11	US-11-130-645B-561328	Sequence 561328,
20	15.2	60.8	64	11	US-11-130-645B-165370	Sequence 165370,
21	15	60.0	64	11	US-11-130-645B-113088	Sequence 113088,
c 22	14.8	59.2	64	11	US-11-130-645B-217720	Sequence 217720,
c 23	14.8	59.2	64	11	US-11-130-645B-542527	Sequence 542527,
c 24	14.8	59.2	64	11	US-11-130-645B-604429	Sequence 604429,
c 25	14.8	59.2	64	11	US-11-130-645B-604559	Sequence 604559,
c 26	14.6	58.4	64	11	US-11-130-645B-333359	Sequence 333359,
c 27	14.6	58.4	64	11	US-11-130-645B-413655	Sequence 413655,
c 28	14.6	58.4	64	11	US-11-130-645B-483536	Sequence 483536,
c 29	14.6	58.4	64	11	US-11-130-645B-537703	Sequence 537703,
c 30	14.6	58.4	64	11	US-11-130-645B-661700	Sequence 661700,
c 31	14.6	58.4	64	11	US-11-130-645B-661823	Sequence 661823,
c 32	14.6	58.4	64	11	US-11-130-645B-661946	Sequence 661946,
c 33	14.6	58.4	64	11	US-11-130-645B-662069	Sequence 662069,
c 34	14.6	58.4	64	11	US-11-130-645B-662743	Sequence 662743,
c 35	14.6	58.4	64	11	US-11-130-645B-717754	Sequence 717754,
c 36	14.6	58.4	62	11	US-11-130-645B-738097	Sequence 738097,
c 37	14.4	57.6	62	11	US-11-130-645B-325028	Sequence 325028,
c 38	14.4	57.6	64	11	US-11-130-645B-112090	Sequence 112090,
c 39	14.4	57.6	64	11	US-11-130-645B-113739	Sequence 113739,
c 40	14.4	57.6	64	11	US-11-130-645B-117452	Sequence 117452,
c 41	14.4	57.6	64	11	US-11-130-645B-155510	Sequence 155510,
c 42	14.4	57.6	64	11	US-11-130-645B-179891	Sequence 179891,
c 43	14.4	57.6	64	11	US-11-130-645B-227807	Sequence 227807,
c 44	14.4	57.6	64	11	US-11-130-645B-367745	Sequence 367745,
c 45	14.4	57.6	64	11	US-11-130-645B-528942	Sequence 528942,

ALIGNMENTS

RESULT 1
US-11-130-645B-528520
Sequence 528520, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: PatentIn version 3.3
SEQ ID NO 528520
LENGTH: 60
TYPE: RNA
ORGANISM: hsa
US-11-130-645B-528520

Query Match 62.4%;   Score 15.6;   DB 11;   Length 60;
Best Local Similarity 54.5%;
Matches 12;   Conservative 6;   Mismatches 4;   Indels 0;   Gaps 0;

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Db  10 UAUUAAGGCACCUGUCACCUUA 31
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RESULT 2
US-11-130-645B-150318
Sequence 150318, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAS AND USES THEREOF
FILE REFERENCE: 06087.0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616
SOFTWARE: PatentIn version 3.3
SEQ ID NO 150318
LENGTH: 63
TYPE: RNA
ORGANISM: hsa
US-11-130-645B-150318

Query Match 62.4%;   Score 15.6;   DB 11;   Length 63;

Qy
Db

Best Local Similarity 59.1%; Conservative 5; Pred. No. 3.1e+02; Indels 0; Gaps 0;
Matches 13;

US-11-130-645B-119663

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Qy  3 TTAAGGGGGCCTGGCCCCTTAAT 24
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Db 24 UUAAGGGGGCCUGCCCUCAUCAU 45
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RESULT 3
US-11-130-645B-119663
Sequence 119663, Application US/11130645B
GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 119663
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa

RESULT 4
US-11-130-645B-139002
Sequence 139002, Application US/11130645B
GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 139002
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-139002

Query Match 62.4%; Score 15.6; DB 11; Length 64;
Best Local Similarity 59.1%; Pred. No. 3.1e+02;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db 22 UUAAGGGGGCCUGCCCUCAUCAU 43
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RESULT 5
US-11-130-645B-178751
Sequence 178751, Application US/11130645B
GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 178751
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-178751

Query Match 62.4%; Score 15.6; DB 11; Length 64;
Best Local Similarity 59.1%; Pred. No. 3.1e+02;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy  3 TTAAGGGGGCCTGGCCCCTTAAT 24
       ::|||||||||:|:|| || :|:
Db 25 UUAAGGGGGCCUGCCCUCAUCAU 46
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; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-178751

Query Match 62.4%; Score 15.6; DB 11; Length 64;
Best Local Similarity 59.1%; Pred. No. 3.1e+02;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db 22 UUAAGGGGGCCUGCCCUCAUCAU 43
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RESULT 6
US-11-130-645B-236152
Sequence 236152, Application US/11130645B
GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 236152
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-236152

Query Match 62.4%; Score 15.6; DB 11; Length 64;
Best Local Similarity 59.1%; Pred. No. 3.1e+02;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy  3 TTAAGGGGGCCTGGCCCCTTAAT 24
       ::|||||||||:|:|| || :|:
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RESULT 7
US-11-130-645B-307585
Sequence 307585, Application US/11130645B
GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 307585
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-307585

Query Match 62.4%; Score 15.6; DB 11; Length 64;
Best Local Similarity 59.1%; Pred. No. 3.1e+02;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy  3 TTAAGGGGGCCTGGCCCCTTAAT 24
       ::|||||||||:|:|| || :|:
Db 22 UUAAGGGGGCCUGCCCUCAUCAU 43
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RESULT 8
US-11-130-645B-333006
Sequence 333006, Application US/11130645B
GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B

; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 333006
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-333006

Query Match   62.4%; Score 15.6; DB 11; Length 64;
Best Local Similarity   59.1%; Pred. No. 3.1e+02;
Matches   13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TTTAAGGGGCCTGGCCCCTTAAT 24
      :::|||||||||||| || |:
Db 25 UUAAGGGGCCUGGCCCCUCAU 46 .

RESULT 9
US-11-130-645B-627039
; Sequence 627039, Application US/11130645B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 627039
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-627039

Query Match   62.4%; Score 15.6; DB 11; Length 64;
Best Local Similarity   59.1%; Pred. No. 3.1e+02;
Matches   13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TTTAAGGGGCCTGGCCCCTTAAT 24
      :::|||||||||||| || |:
Db 22 UUAAGGGGCCUGCCCCUCAU 43

RESULT 10
US-11-130-645B-688578
; Sequence 688578, Application US/11130645B
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; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 688578
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-688578

Query Match   62.4%; Score 15.6; DB 11; Length 64;
Best Local Similarity   59.1%; Pred. No. 3.1e+02;
Matches   13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TTTAAGGGGCCTGGCCCCTTAAT 24
      :::|||||||||||| || |:
Db 25 UUAAGGGGCCUGCCCUCAUCAU 46

RESULT 11
US-11-130-645B-1115601/c
; Sequence 115601, Application US/11130645B

; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 115601
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-115601

Query Match   61.6%; Score 15.4; DB 11; Length 64;
Best Local Similarity   94.1%; Pred. No. 4e+02;
Matches   16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AAGGGGCCTGGCCCCTT 21
      |||||||||| |||||||
Db 19 AAGGGGCCUGCCCCCTT 3

RESULT 12
US-11-130-645B-235099/c
; Sequence 235099, Application US/11130645B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 235099
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-235099

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Best Local Similarity   94.1%; Pred. No. 4e+02;
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RESULT 13
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; Sequence 378454, Application US/11130645B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 378454
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-378454

Query Match   61.6%; Score 15.4; DB 11; Length 64;
Best Local Similarity   94.1%; Pred. No. 4e+02;
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; Sequence 378526, Application US/11130645B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 378526
; LENGTH: 64
; TYPE: RNA
; ORGANISM: hsa
US-11-130-645B-378526

Query Match   61.6%;   Score 15.4; DB 11; Length 64;
Best Local Similarity   94.1%;   Pred. No. 4e+02;
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Qy   5 AAGGGGGCCTGGCCCCCTT 21
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Db   22 AAGGGGGCCTGCCCCCTT 6

RESULT 15
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; Sequence 427234, Application US/11130645B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: MICRORNAS AND USES THEREOF
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645B
; CURRENT FILING DATE: 2005-05-16
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; SOFTWARE: Patentin version 3.3
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; TYPE: RNA
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US-11-130-645B-427234

Query Match   61.6%;   Score 15.4; DB 11; Length 64;
Best Local Similarity   94.1%;   Pred. No. 4e+02;
Matches 16; Conservative   0; Mismatches 1; Indels   0; Gaps   0;

Qy   5 AAGGGGGCCTGGCCCCCTT 21
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Search completed: February 7, 2006, 12:30:41
Job time : 164 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: February 7, 2006, 11:18:34 ; Search time 3629 Seconds
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Title: US-10-613-390B-1
Perfect score: 25
Sequence: 1 tattaagggcctggcccttaata 25

Scoring table: IDENTITY NUC
                     Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 2764578925 residues

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Post-processing: Minimum Match 0%
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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	100.0	25	53	US-10-613-390B-1	Sequence 1, Appli
3	23.4	25	1	PCT-US03-20696-7	Sequence 7, Appli
4	93.6	25	53	US-10-613-390B-1	Sequence 1, Appli
5	17.4	25	62	US-10-809-189-116728	Sequence 116728,
6	17.2	25	38	US-09-956-584A-366654	Sequence 366654,
7	17.2	25	38	US-09-956-604-22327	Sequence 22327, A
8	17.2	25	38	US-09-956-604A-22327	Sequence 22327, A
9	17.2	25	38	US-09-956-604B-22327	Sequence 22327, A
10	17.2	25	77	US-60-234-049-56273	Sequence 56273, A
11	17	25	35	US-09-498-485A-1998	Sequence 1998, Ap
12	17	25	35	US-09-912-293-44099	Sequence 44099, A
13	17	25	24	US-09-498-485A-4160	Sequence 4160, Ap
14	16.4	25	24	US-09-498-485A-4160	Sequence 4160, Ap
15	16.4	25	35	US-09-912-293-117317	Sequence 117317,
16	16.2	25	81	US-10-956-160-52224	Sequence 52224, A
17	16.2	25	64	US-09-912-293-117317	Sequence 117317,
18	16.2	25	71	US-11-130-645A-561328	Sequence 561328,
19	16.2	25	64	US-11-130-645A-165370	Sequence 165370,
20	16	25	53	US-10-605-923-1462089	Sequence 1462089,
21	16	25	49	US-10-310-914A-1296097	Sequence 1296097,
22	16	23	49	US-10-605-924-1296097	Sequence 1296097,
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ALIGNMENTS

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26	15.8	63.2	21	49	US-10-310-914A-621697	Sequence 621697,
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29	15.8	63.2	21	53	US-10-605-924-621697	Sequence 621697,
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33	15.8	63.2	23	55	US-10-355-577-621452	Sequence 621452,
34	15.8	63.2	49	60	US-10-719-900-27015	Sequence 27015, A
35	15.8	63.2	25	60	US-11-036-317-27016	Sequence 27016, A
36	15.8	63.2	25	62	US-10-809-189-116728	Sequence 116728,
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RESULT 1
PCT-US03-20696-7
; Sequence 7, Application PC/TUS0320696
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning, Inc.
; APPLICANT: Zhifang Zhu
; APPLICANT: Yuliang Cui
; APPLICANT: Qingqing Ding
; APPLICANT: Li Li
; APPLICANT: Zhi Wang
; TITLE OF INVENTION: Oligonucleotides for Treating
; TITLE OF INVENTION: Proliferative Disorders
; FILE REFERENCE: 13552PCT
; CURRENT APPLICATION NUMBER: PCT/US03/20696
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/400,137
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: (0)...(0)
; OTHER INFORMATION: found in any organism
; FEATURE:
; OTHER INFORMATION: found in any organism
US-10-613-390B-1

Query Match   100.0%;   Score 25;   DB 1;   Length 25;
Best Local Similarity   100.0%;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 TATTAAGGGGGCCTGGCCCCCTTAATA 25
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Db   1 TATTAAGGGGGCCTGGCCCCCTTAATA 25

RESULT 2
US-10-613-390B-1
; Sequence 1, Application US/10613390B
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning Inc
; TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders

; FILE REFERENCE: 60/400,137
; CURRENT APPLICATION NUMBER: US/10/613,390B
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10/613390
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic primer
US-10-613-390B-1

Query Match   100.0%;   Score 25;   DB 53;   Length 25;
Best Local Similarity   100.0%;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 TATTAAGGGGGCCTGGCCCCCTTAATA 25
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RESULT 3
PCT-US03-20696-7/c
; Sequence 7, Application PC/TUS0320696
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning, Inc.
; APPLICANT: Zhifang Zhu
; APPLICANT: Yuliang Cui
; APPLICANT: Qingqing Ding
; APPLICANT: Li Li
; APPLICANT: Zhi Wang
; TITLE OF INVENTION: Oligonucleotides for Treating
; TITLE OF INVENTION: Proliferative Disorders
; FILE REFERENCE: 13552PCT
; CURRENT APPLICATION NUMBER: PCT/US03/20696
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/400,137
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: (0)...(0)
; OTHER INFORMATION: found in any organism
; FEATURE:
; OTHER INFORMATION: found in any organism
PCT-US03-20696-7

Query Match   93.6%;   Score 23.4;   DB 1;   Length 25;
Best Local Similarity   96.0%;
Matches   24; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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; Sequence 1, Application US/10613390B
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning Inc
; TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders
; FILE REFERENCE: 60/400,137
; CURRENT APPLICATION NUMBER: US/10/613,390B
; CURRENT FILING DATE: 2003-07-03

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;   SOFTWARE: Patentin version 3.2
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;   SEQ ID NO 1
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;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic primer
US-10-613-390B-1

Qy   1 TATTAAGGGGGGCCCTGGCCCCCTTAATA 25
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Query Match        93.8%;  Score 23.4;  DB 53;  Length 25;
Best Local Similarity  96.0%;  Pred. No. 25;
Matches   24;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

RESULT 5
US-10-809-189-116728/c
Sequence 116728, Application US/10809189
;   GENERAL INFORMATION:
;   APPLICANT: Michael Mittmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/10/809,189
;   CURRENT FILING DATE: 2004-03-25
;   PRIOR APPLICATION NUMBER: US/09/396,196
;   PRIOR FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 116728
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-10-809-189-116728

Qy   6 AGGGGCCCTGGCCCCCTTAAT 24
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Db  25 AGGGGCCCTGGCACCTTAAT 7

Query Match        69.6%;  Score 17.4;  DB 62;  Length 25;
Best Local Similarity  94.7%;  Pred. No. 9.5e+03;
Matches   18;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

RESULT 6
US-09-956-584A-366654/c
Sequence 366654, Application US/0995584A
;   GENERAL INFORMATION:
;   APPLICANT: Mittmann, Michael
;   TITLE OF INVENTION: Genetic Analysis of Mouse
;   FILE REFERENCE: 3115.1
;   CURRENT APPLICATION NUMBER: US/09/956,584A
;   CURRENT FILING DATE: 2001-09-19
;   PRIOR APPLICATION NUMBER: 60/234,017
;   PRIOR FILING DATE: 2000-09-20
;   NUMBER OF SEQ ID NOS: 605887
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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US-09-956-584A-366654
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Best Local Similarity  86.4%;  Pred. No. 1.2e+04;
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US-09-956-604-22327

RESULT 7
US-09-956-604-22327/c
Sequence 22327, Application US/0995604
;   GENERAL INFORMATION:
;   APPLICANT: Mittmann, Michael
;   TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
;   FILE REFERENCE: 3117.1
;   CURRENT APPLICATION NUMBER: US/09/956,604
;   CURRENT FILING DATE: 2001-09-19
;   PRIOR APPLICATION NUMBER: 60/234,049
;   PRIOR FILING DATE: 2000-09-19
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;   ORGANISM: Escherichia coli
US-09-956-604-22327

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Query Match        68.8%;  Score 17.2;  DB 38;  Length 25;
Best Local Similarity  86.4%;  Pred. No. 1.2e+04;
Matches   19;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

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;   TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
;   FILE REFERENCE: 3117.1
;   CURRENT APPLICATION NUMBER: US/09/956,604A
;   PRIOR APPLICATION NUMBER: US/09/956,604A
;   PRIOR FILING DATE: 2001-09-19
;   PRIOR APPLICATION NUMBER: 60/234,049
;   PRIOR FILING DATE: 2000-09-19
;   NUMBER OF SEQ ID NOS: 141629
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-09-956-604A-22327

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       ||||||| ||| ||| ||||||
Db  24 TATTAACGGGCTTGGGTCCCTTA 3

Query Match        68.8%;  Score 17.2;  DB 38;  Length 25;
Best Local Similarity  86.4%;  Pred. No. 1.2e+04;
Matches   19;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

RESULT 9
US-09-956-604B-22327/c
Sequence 22327, Application US/0995604B
;   GENERAL INFORMATION:
;   APPLICANT: Mittmann, Michael
;   TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
;   FILE REFERENCE: 3117.1
;   CURRENT APPLICATION NUMBER: US/09/956,604B
```

```
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 22327
TYPE: DNA
LENGTH: 25
ORGANISM: Escherichia coli
US-09-956-604B-22327

Qy    1 TATTAAGGGGCCTGGGCCCCCTTA 22
          ||||| ||||| |  |||||||||
Db   24 TATTAACGGGCTTGGTCCCTTA 3

Query Match 68.8%; Score 17.2; DB 38; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
US-09-956-604B-22327

RESULT 10
US-60-234-049-56273/c
Sequence 56273, Application US/60234049
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Escherichia coli
FILE REFERENCE: 3117
CURRENT APPLICATION NUMBER: US/60/234,049
CURRENT FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56273
LENGTH: 25
TYPE: DNA
ORGANISM: Escherichia coli
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-56273

Query Match 68.8%; Score 17.2; DB 77; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy    1 TATTAAGGGGCCTGGGCCCCCTTA 22
          ||||| ||||| |  |||||||||
Db   24 TATTAACGGGCTTGGTCCCTTA 3

RESULT 11
US-09-498-485A-1998
Sequence 1998, Application US/09498485A
GENERAL INFORMATION:
APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 46
FILE REFERENCE: PO46
CURRENT APPLICATION NUMBER: US/09/498,485A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/118,775
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 8166
SEQ ID NO 1998
LENGTH: 99
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (39)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (61)
OTHER INFORMATION: n equals a,t,g, or c
```

```
NAME/KEY: misc_feature
LOCATION: (66)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (73)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (98)
OTHER INFORMATION: n equals a,t,g, or c
US-09-498-485A-1998

Query Match 68.0%; Score 17; DB 24; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy    1 TATTAAGGGGCCTGGGCCCCCTTAATA 25
          |||||||||||||||||| ||| | |
Db    9 TGTTAAGGGGCGGGCCTGGGCGTCTTGAAA 33

RESULT 12
US-09-912-293-44099
Sequence 44099, Application US/09912293
GENERAL INFORMATION:
APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
FILE REFERENCE: PO-100
CURRENT APPLICATION NUMBER: US/09/912,293
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 08/103,744
PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 09/249,651
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 08/104,507
PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 08/196,363
PRIOR FILING DATE: 1994-02-15
PRIOR APPLICATION NUMBER: 08/221,623
PRIOR FILING DATE: 1994-03-31
PRIOR APPLICATION NUMBER: 08/859,490
PRIOR FILING DATE: 1994-03-31
PRIOR APPLICATION NUMBER: 08/220,691
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 08/196,362
PRIOR FILING DATE: 1994-03-31
PRIOR APPLICATION NUMBER: 09/741,830
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/813,155
PRIOR FILING DATE: 2001-03-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 244538
SEQ ID NO 44099
LENGTH: 99
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (39)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (61)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66)..(66)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (73)..(73)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
```

RESULT 13
US-09-498-485A-4160
; Sequence 4160, Application US/0949485A
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 46
; FILE REFERENCE: PO46
; CURRENT APPLICATION NUMBER: US/09/498,485A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/118,775
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 8166
; SEQ ID NO 4160
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (19)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (27)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (29)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (71)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (82)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (92)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-498-485A-4160

Query Match 68.0%; Score 17; DB 35; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy  1 TATTAAGGGGGGCCTGGCCCCCTTAATA 25
       |||||||||||||||||||| |||||| |
Db  9 TGTTAAGGGGGGCCTGGCCGGTCTTGAAA 33
```

US-09-912-293-44099

RESULT 14
US-09-498-485A-4160/c
; Sequence 4160, Application US/0949485A
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.

Query Match 65.6%; Score 16.4; DB 24; Length 99;
Best Local Similarity 94.4%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy  1 TATTAAGGGGGGCCTGGCCCC 18
       |||||||||||||||| |||||
Db 43 TATTAAGGGGGGCCCGGCGCC 60
```

RESULT 15
US-09-912-293-117317
; Sequence 117317, Application US/0991229A
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
; FILE REFERENCE: PO-100
; CURRENT APPLICATION NUMBER: US/09/912,293
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 08/103,744
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 08/103,744
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 09/249,651
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 08/104,507
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 08/196,363
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 09/859,490
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 08/196,362
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 08/221,623
; PRIOR FILING DATE: 1994-03-31
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 46
; FILE REFERENCE: PO46
; CURRENT APPLICATION NUMBER: US/09/498,485A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/118,775
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 8166
; SEQ ID NO 4160
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (19)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (27)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (29)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (71)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (82)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (92)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-498-485A-4160

Query Match 65.6%; Score 16.4; DB 24; Length 99;
Best Local Similarity 94.4%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy  8 GGGCCTGGCCCCCTTAATA 25
       ||||| |||||||||||||
Db 60 GGGCCGGCGCCCCTTAATA 43
```

```
;  PRIOR APPLICATION NUMBER: 08/220,691
;  PRIOR FILING DATE: 1994-03-31
;  PRIOR APPLICATION NUMBER: 09/741,830
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 09/813,155
;  PRIOR FILING DATE: 2001-03-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 244538
;  SEQ ID NO 117317
;    LENGTH: 99
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (8)..(8)
;    OTHER INFORMATION: n is equal to a,t,g, or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (19)..(19)
;    OTHER INFORMATION: n is equal to a,t,g, or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (25)..(27)
;    OTHER INFORMATION: n is equal to a,t,g, or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (29)..(29)
;    OTHER INFORMATION: n is equal to a,t,g, or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (71)..(71)
;    OTHER INFORMATION: n is equal to a,t,g, or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (82)..(82)
;    OTHER INFORMATION: n is equal to a,t,g, or c
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (92)..(92)
;    OTHER INFORMATION: n is equal to a,t,g, or c
US-09-912-293-117317

Query Match             65.6%;  Score 16.4;  DB 35;  Length 99;
Best Local Similarity   94.4%;  Pred. No. 2.8e+04;
  Matches   17;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy          1 TATTAAGGGGCCCTGGCCC 18
              |||||||||||||| |||||
Db         43 TATTAAGGGGCCCCGGCCC 60
```

Search completed: February 7, 2006, 12:27:52
Job time : 3631 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration ltd.

Run on: February 7, 2006, 10:53:05 ; Search time 272 Seconds

Title: US-10-613-390B-1
Perfect score: 25
Sequence: 1 tattaagggggcctggcccctaata 25
Scoring table: IDENTITY.NUC
                Gapop 10.0 , Gapext 1.0
Searched: 4996997 seqs, 333246308 residues
Total number of hits satisfying chosen parameters: 5288460

Minimum DB seq length: 0
Maximum DB seq length: 100
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

612.564 Million cell updates/sec (without alignments)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	25	100.0	25	12	ADK67857	Adk67857 Transcrip
c 2	23.4	93.6	25	12	ADK67857	Adk67857 Transcrip
3	15.8	63.2	51	12	AAL30340	Aal30340 Human SNP
c 4	15.4	61.6	50	4	AAL31509	Aal31509 Human SNP
c 5	15.4	61.6	50	4	AAL31507	Aal31507 Human SNP
c 6	15	60.0	90	14	ACL62385	Acl62385 Human col
c 7	14.4	57.6	70	2	AAT71443	Aat71443 Glioblast
c 8	14.2	56.8	31	3	AAA78645	Aaa78645 Human gen
c 9	14.2	56.8	49	2	AAQ69655	Aaq69655 Human gen
c 10	14.2	56.8	49	2	AAQ69655	Aaq69655 Human ade
c 11	14.2	56.8	49	2	AAT64117	Aat64117 Human ade
c 12	14.2	56.8	49	2	AAT64117	Aat64117 Human ade
c 13	14.2	56.8	49	2	AAX17405	Aax17405 Test sequ
c 14	14.2	56.8	49	6	AAX17405	Aax17405 Test sequ
c 15	14.2	56.8	49	6	ABK82896	Abk82896 DNA bindi
c 16	14.2	56.8	49	6	ABK82896	Abk82896 DNA bindi
c 17	14.2	56.8	49	12	ADE80435	Ade80435 Duplex ol
c 18	14.2	56.8	49	12	ADE80435	Ade80435 Duplex ol
c 19	14.2	56.8	51	4	AAL30340	Aal30340 Human SNP
c 20	14	56.0	63	2	AAX04573	Aax04573 PCR prime
c 21	14	56.0	63	10	AAZ11454	Aazl1454 Wild-type
c 22	13.8	55.2	21	10	ADD94048	Add94048 PCR prime
c 23	13.8	55.2	21	10	ADD94058	Add94058 PCR prime
c 24	13.8	55.2	25	9	ACK17136	Ack17136 Human mic
c 25	13.8	55.2	25	9	ACK17137	Ack17137 Human mic
c 26	13.8	55.2	37	12	ADK17981	Adk17981 Saturatio
c 27	13.8	55.2	37	12	ADK17982	Adk17982 Saturatio
c 28	13.8	55.2	37	12	ADJ53933	Adj53933 Site satu
c 29	13.8	55.2	37	12	ADJ53934	Adj53934 Site satu
c 30	13.8	55.2	45	8	ABT34022	Abt34022 Human pig
c 31	13.8	55.2	50	4	AAL31509	Aal31509 Human SNP
c 32	13.8	55.2	51	4	AAL31507	Aal31507 Human SNP
c 33	13.8	55.2	61	3	AAC11080	Aac11080 Human sec
c 34	13.8	55.2	83	4	AAI27785	Aai27785 Probe #17
c 35	13.8	55.2	83	4	ABA76096	Aba76096 Human foe
c 36	13.8	55.2	83	4	AAK24770	Aak24770 Human bra
c 37	13.8	55.2	83	6	ABS24246	Abs24246 Human gen
c 38	13.8	55.2	83	6	ABS24246	Abs24246 Human gen
c 39	13.6	54.4	22	10	ADJ95320	Adj95320 Novel NOV
c 40	13.6	54.4	30	14	ADJ11539	Adj11539 Human col
c 41	13.6	54.4	32	5	AAF61993	Aaf61993 K. maxia
c 42	13.6	54.4	42	6	ABL95768	Abl95768 Rat GALP-
c 43	13.6	54.4	49	10	ADB67044	Adb67044 Mouse Gal
c 44	13.6	54.4	68	12	ADM87895	Adm87895 Gene expr
c 45	13.6	54.4	70	14	ADZ27716	Adz27716 Chemosens

ALIGNMENTS

RESULT 1
ADK67857

ID   ADK67857 standard; DNA; 25 BP.
XX
AC   ADK67857;
XX
DT   06-MAY-2004   (first entry)
XX
DE   Transcription activator-binding oligonucleotide (oligo #2).
XX
KW   Cytostatic; lung cancer; melanoma; leukaemia; gene therapy; ss.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   TATA_signal   1..6
FT   /*tag= a
FT   GC_signal   7..12
FT   /*tag= b
XX
PN   WO200401265A-A2.
XX
PD   12-FEB-2004.
XX
PF   30-JUN-2003; 2003WO-US020696.
XX
PR   01-AUG-2002; 2002US-0400137P.
XX
PA   (GENE-) GENE CLONING INC.
XX
PI   Zhu Z, Cui Y, Ding Q, Li L, Wang Z;
XX
DR   WPI; 2004-156997/15.
XX
PT   Treating a proliferative disorder in a subject comprises administering a
PT   proliferation-inhibiting amount of a single-stranded oligonucleotide
PT   capable of binding to one or more DNA-binding proteins or RNA primers in
PT   the subject.
XX
PS   Example 21; SEQ ID NO 7; 36pp; English.
XX
CC   The present sequence is that of oligo #2, a 25-mer single-stranded

CC   oligonucleotide that includes a TATA signal and GC signal sequence. Oligo
CC   #2 is used in a claimed method of modulating transcription in a cell. The
CC   invention provides compositions and methods for treating a proliferative
CC   disorder, in particular lung cancer, melanoma or leukaemia (claimed),
CC   comprising administering a proliferation-inhibiting amount of a single-
CC   stranded oligonucleotide that is capable of binding to one or more DNA-
CC   binding proteins or RNA primers. In an example from the invention, mice
CC   were administered p388 leukaemia cancer cells by i.p. injection and then
CC   received i.v. injections of oligo #2 and/or oligo #4 (a 7-mer random
CC   oligo DNA). Results showed that oligo #2 at a dosage of 1 mg/kg/day i.v.
CC   with oligo #4 at 1 mg/kg/day i.v. attained perfect results, up to 36 days
CC   after cancer cell injection, with a 100% survival rate. The 7-mer alone
CC   attained a 60% survival rate. The results showed that oligo #2 could
CC   interfere with RNA transcription.
XX
SQ   Sequence 25 BP; 6 A; 6 C; 6 G; 7 T; 0 U; 0 Other;

Qy
Db

  Qy   1 TATTAAGGGGCGCCTGGGCCCCCTTAATA 25
                |||||||||||||||||||||||||||||
  Db   1 TATTAAGGGGCGCCTGGGCCCCCTTAATA 25

Query Match   100.0%;   Score 25;   DB 12;   Length 25;
Best Local Similarity 100.0%;   Pred. No. 0.01;
Matches   25;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 2
ADK67857/c
ID   ADK67857 standard; DNA; 25 BP.
XX
AC   ADK67857;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Transcription activator-binding oligonucleotide (oligo #2).
XX
KW   Cytostatic; lung cancer; melanoma; leukaemia; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   TATA_signal   1..6
FT   /*tag= a
FT   7..12
FT   GC_signal   /*tag= b
XX
PN   WO2004012654-A2.
XX
PD   12-FEB-2004.
XX
PF   30-JUN-2003; 2003WO-US020696.
XX
PR   01-AUG-2002; 2002US-0400137P.
XX
PA   (GENE-) GENE CLONING INC.
XX
PI   Zhu Z, Cui Y, Ding Q, Li L, Wang Z;
XX
DR   WPI; 2004-156997/15.
XX
PT   Treating a proliferative disorder in a subject comprises administering a
PT   proliferation-inhibiting amount of a single-stranded oligonucleotide
PT   capable of binding to one or more DNA-binding proteins or RNA primers in
PT   the subject.
XX
PS   Example 21; SEQ ID NO 7; 36pp; English.
XX
CC   The present sequence is that of oligo #2, a 25-mer single-stranded
CC   oligonucleotide that includes a TATA signal and GC signal sequence. Oligo
CC   #2 is used in a claimed method of modulating transcription in a cell. The
CC   invention provides compositions and methods for treating a proliferative
CC   disorder, in particular lung cancer, melanoma or leukaemia (claimed),
CC   comprising administering a proliferation-inhibiting amount of a single-

CC   stranded oligonucleotide that is capable of binding to one or more DNA-
CC   binding proteins or RNA primers. In an example from the invention, mice
CC   were administered p388 leukaemia cancer cells by i.p. injection and then
CC   received i.v. injections of oligo #2 and/or oligo #4 (a 7-mer random
CC   oligo DNA). Results showed that oligo #2 at a dosage of 1 mg/kg/day i.v.
CC   with oligo #4 at 1 mg/kg/day i.v. attained perfect results, up to 36 days
CC   after cancer cell injection, with a 100% survival rate. The 7-mer alone
CC   attained a 60% survival rate. The results showed that oligo #2 could
CC   interfere with RNA transcription.
XX
SQ   Sequence 25 BP; 6 A; 6 C; 6 G; 7 T; 0 U; 0 Other;

Qy
Db

  Qy   1 TATTAAGGGGCGCCTGGGCCCCCTTAATA 25
                ||||||||||||||||| ||||||||||||
  Db   25 TATTAAGGGGCGCCCAGGGCCCCCTTAATA 1

Query Match   93.6%;   Score 23.4;   DB 12;   Length 25;
Best Local Similarity 96.0%;   Pred. No. 0.065;
Matches   24;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

RESULT 3
AAL30340/c
ID   AAL30340 standard; DNA; 51 BP.
XX
AC   AAL30340;
XX
DT   24-JAN-2002 (first entry)
XX
DE   Human SNP oligonucleotide #3548.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035498.
XX
PR   28-DEC-1999; 99US-0173419P.
PR   27-DEC-2000; 2000US-0017341.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA, Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT   autoimmune diseases and infections.
XX
PS   Claim 1; Page 2404; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, interferons, oncogenes,
CC   proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-
CC   protein coupled receptors and thioesterases. The present sequence is one
CC   such oligonucleotide. The oligonucleotides and the peptides encoded by
CC   them may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate expression of the proteins listed above.
CC   Disorders that may be prevented, diagnosed and/or treated include

RESULT 4
AAL31509/c
ID   AAL31509 standard; DNA; 50 BP.
XX
AC   AAL31509;
XX
DT   24-JAN-2002 (first entry)
XX
DE   Human SNP oligonucleotide #4717.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   interleukin; G-protein coupled receptor; cytochrome; kinesin; interferon;
KW   complement related protein; cytokine; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035498.
XX
PR   28-DEC-1999; 99US-0173419P;
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA, Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT   autoimmune diseases and infections.
XX
PS   Claim 1; Page 2743; 4143pp; English.

CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherins, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC   protein coupled receptors and thioesterases. The present sequence is one
CC   such oligonucleotide. The oligonucleotides and the peptides encoded by
CC   them may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate expression of the proteins listed above.
CC   Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms

SQ   Sequence 51 BP; 14 A; 16 C; 18 G; 3 T; 0 U; 0 Other;

Query Match   63.2%; Score 15.8; DB 4; Length 51;
Best Local Similarity   89.5%;
Matches   17; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 TATTAAGGGGGGCCTGGGCCCC 19
              ||||| ||||||||||||||||
Db   31 TTTTAGGGGGGCCTGGGCCCC 13

RESULT 5
AAL31507/c
ID   AAL31507 standard; DNA; 50 BP.
XX
AC   AAL31507;
XX
DT   24-JAN-2002 (first entry)
XX
DE   Human SNP oligonucleotide #4715.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   interleukin; G-protein coupled receptor; cytochrome; kinesin; interferon;
KW   complement related protein; cytokine; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035498.
XX
PR   28-DEC-1999; 99US-0173419P;
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA, Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT   autoimmune diseases and infections.
XX
PS   Claim 1; Page 2743; 4143pp; English.

CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherins, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC   protein coupled receptors and thioesterases. The present sequence is one
CC   such oligonucleotide. The oligonucleotides and the peptides encoded by
CC   them may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate expression of the proteins listed above.
CC   Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms

SQ   Sequence 50 BP; 8 A; 17 C; 19 G; 6 T; 0 U; 0 Other;

Query Match   61.6%; Score 15.4; DB 4; Length 50;
Best Local Similarity   94.1%;
Matches   16; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   4 TAAGGGGGGCCTGGGCCCCT 20
              |||||||||||||||||| |
Db   18 TAAGGGGGGCCTGGGCCACT 2

RESULT 6
ACL62385

ID   ACL62385 standard; cDNA; 90 BP.
XX
AC   ACL62385;
XX
DT   24-MAR-2005 (first entry)
XX
DE   Human colon cancer differentially expressed polynucleotide, SEQ ID:8520.
XX
KW   Differential expression; diagnosis; therapy; drug screening; cancer;
KW   neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;
KW   ss.
XX
OS   Homo sapiens.
XX
XX
PN   WO2005000087-A2.
XX
PD   06-JAN-2005.
XX
PF   13-MAY-2004; 2004WO-US015421.
XX
PR   03-JUN-2003; 2003US-0475872P.
XX
PA   (CHIR) CHIRON CORP.
XX
PI   Randazzo F, Moler B, Escobedo J, Garcia PD;
XX
DR   WPI; 2005-075421/08.
XX
PT   New isolated polynucleotides, which are differentially expressed in colon
PT   cancer cell, useful for treating cancer, e.g. colon cancer, breast
PT   cancer, or pancreatic cancer.
XX
PS   Claim 1; SEQ ID NO 8520; 97pp; English.
XX
CC   The invention relates to 9672 polynucleotides (ACL53866-ACL63537) which
CC   are differentially expressed in colon cancer cells. The invention also
CC   relates to vectors and host cells comprising a differentially expressed
CC   polynucleotide of the invention; a method for detecting a cancerous cell
CC   by detection of a gene product of the polynucleotide; a method for
CC   inhibiting a cancerous phenotype of a cell by inhibiting a gene product
CC   of the polynucleotides; a method of treating an individual with cancer by
CC   administration of a modulator of a gene product of the polynucleotides;
CC   and an isolated antibody that specifically binds to a polypeptide encoded
CC   by one of the 9672 polynucleotides. The polynucleotides, polypeptides,
CC   antibodies, and methods are useful for the detection of cancerous cells;
CC   for the diagnosis, prognosis and management of cancer; for the
CC   identification of agents that modulate the phenotype of cancerous cells;
CC   and for the treatment of cancer, especially colon cancer and metastasized
CC   colon cancer, but also breast or pancreatic cancer. The polynucleotides
CC   are also useful as a source of probes or primers for use in diagnostic
CC   methods. The differentially expressed polynucleotides or their encoded
CC   proteins can additionally be used as vaccines to modulate primary immune
CC   responses for the prevention or treatment of cancer. The present sequence
CC   represents a specifically claimed polynucleotide which is differentially
CC   expressed in colon cancer. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 50 BP; 8 A; 14 C; 22 G; 6 T; 0 U; 0 Other;

Query Match   61.6%; Score 15.4; DB 4; Length 50;
Best Local Similarity   94.1%;
Matches   16; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   4 TAAGGGGCCTGGCCCCT 20
              |||||||||||||| ||
Db   44 TAAGGGGCCTGGCCACT 28

RESULT 7
AAT71443/c

ID   AAT71443 standard; DNA; 70 BP.
XX
AC   AAT71443;
XX
DT   01-AUG-1997 (first entry)
XX
DE   Glioblastoma U251 cell line ligand GBI.86.
XX
KW   Ligand; glioblastoma; brain; tumour; SELEX; in vivo; imaging;
KW   systematic evolution of ligands by exponential enrichment; cancer;
KW   drug delivery; cell line; ss.
XX
OS   Synthetic.
XX
XX
PN   WO9634875-A1.
XX
PD   07-NOV-1996.
XX
PF   01-MAY-1996; 96WO-US006060.
XX
PR   03-MAY-1995; 95US-00433585.
PR   03-MAY-1995; 95US-00434001.
PR   03-MAY-1995; 95US-00434425.
PR   03-MAY-1995; 95US-00437667.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
PA   (UYRE-) UNIV RES CORP.
XX
PI   Jensen KB, Chen H, Morris KN, Stephens A, Gold L;
XX
DR   WPI; 1996-506092/50.
XX
PT   Identifying nucleic acid ligands for tissues - by contacting candidate
PT   mixt. of nucleic acids with tissue and enriching for increased affinity
PT   nucleic acids.
XX
PS   Claim 22; Page 70; 110pp; English.
XX
CC   The present sequence is a single stranded DNA ligand to the human brain
CC   tumour derived, glioblastoma U251 cell line, prepared by systematic
CC   evolution of ligands by exponential enrichment (SELEX). A single stranded
CC   DNA pool was incubated with U251 cells, and the tighter binding sequences
CC   partitioned from the rest of the pool by filtering the reaction through
CC   nitrocellulose filters. Twenty rounds of selection were carried out,
CC   using a decreasing concentration of U251 cells can be used in vivo to image
CC   ligands to glioblastoma cell lines as the SELEX progressed.
CC   glioblastomas, and for the therapeutic localisation of the ligand or
CC   other attached therapeutic agents
XX
SQ   Sequence 90 BP; 21 A; 32 C; 22 G; 15 T; 0 U; 0 Other;

Query Match   60.0%; Score 15; DB 14; Length 90;
Best Local Similarity   78.3%;
Matches   18; Conservative   0; Mismatches   5; Indels   0; Gaps   0;

Qy   3 TTAAGGGGCCTGGCCCCTTAATA 25
              ||||||||||| ||| ||||||
Db   35 TTAAGGGGCGGTTGGGCCCTGAAGA 57

SQ   Sequence 70 BP; 11 A; 20 C; 14 G; 25 T; 0 U; 0 Other;

Query Match   57.6%; Score 14.4; DB 2; Length 70;
Best Local Similarity   75.0%;
Matches   18; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   2 ATTAAGGGGCCTGGCCCCTTAATA 25
              ||||||||||||||| |||||
Db   60 AATAAGCGGCCCTGGAGCTTTAACA 37

RESULT 8
ID   AAA78645 standard; DNA; 31 BP.
XX
AC   AAA78645;
XX
DT   20-NOV-2000 (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag SEQ ID NO:15.
XX
KW   Human; genomic DNA; polymorphism; genome; allele-specific; primer; probe;
KW   hybridisation; polymorphic site; forensic; paternity testing; medicine;
KW   phenotypic trait; genetic analysis; genetic mapping; ds.
XX
OS   Homo sapiens.
XX
PN   EP1024200-A2.
XX
PD   02-AUG-2000.
XX
PF   26-JAN-2000; 2000EP-00250023.
XX
PR   27-JAN-1999; 99US-00238402.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Patil N, Shah N, Warrigton JA;
XX
DR   WPI; 2000-500198/45.
XX
PT   Human genomic polymorphic nucleic acid segments, allele specific primers
PT   and probes, and methods of analysis, useful for e.g. forensics, paternity
PT   testing, genetic mapping..
XX
PS   Claim 1; Page 5; 141pp; English.
XX
CC   The present invention describes a nucleic acid segment of 10-100
CC   contiguous bases chosen from one of 632 fragments (AAA78631 to AAA79262),
CC   where the segment comprises a polymorphic site or an immediately adjacent
CC   base, or the complement of the segment. Also described are: (1) an allele
CC   -specific oligonucleotide that hybridises to a segment of the novelty;
CC   (2) an isolated nucleic acid comprising a sequence of the novelty where
CC   the polymorphic site within the sequence is occupied by a base other than
CC   the reference base indicated in the specification; and (3) analysing a
CC   nucleic acid, comprising obtaining a nucleic acid from an individual, and
CC   determining a base occupying any one of the polymorphic sites of the
CC   novelty. The nucleic acid segments and method can be used to analyse an
CC   individuals nucleic acid sequences for the presence of polymorphisms. The
CC   method can also be used to test for a disease phenotype and correlate the
CC   presence of the phenotype with a particular polymorphism. The presence of
CC   polymorphic sites are useful for, e.g. forensics, paternity testing,
CC   correlation of polymorphisms with phenotypic traits and for genetic
CC   mapping of phenotypic traits. AAA78631 to AAA79262 represent sequence
CC   tags of human genomic DNA fragments containing polymorphic sites. The
CC   base occupying the polymorphic site is indicated using IUPAC-IUB
CC   nomenclature
XX
SQ   Sequence 31 BP; 3 A; 8 C; 8 G; 11 T; 0 U; 1 Other;

Query Match   56.8%; Score 14.2; DB 3; Length 31;
Best Local Similarity   76.2%;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy   1 TATTAAGGGCCTGGCCCCTT 21
             |||:||:||| |||||| |||
Db   9 TCTTCAGRGGACTGGCTCCTT 29

XX

RESULT 9
ID   AAQ69655 standard; DNA; 49 BP.
XX

AC   AAQ69655;
XX
DT   25-MAR-2003 (revised)
DT   01-MAR-1995 (first entry)
XX
DE   Human adenosine deaminase gene, target region.
XX
KW   DNA protein-binding assay; test sequence; screening sequence; promoter;
KW   target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9;
KW   transcription factor; TFIID; ds.
XX
OS   Synthetic.
XX
PN   WO9414980-A1.
XX
PD   07-JUL-1994.
XX
PF   20-DEC-1993; 93WO-US012388.
XX
PR   23-DEC-1992; 92US-00996783.
PR   17-SEP-1993; 93US-00123936.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;
XX
DR   WPI; 1994-234711/28.
XX
PT   Sequence-directed DNA-binding molecules - useful in pharmaceuticals and
PT   as molecular reagents.
XX
PS   Claim 28; Page 414; 587pp; English.
XX
CC   A DNA protein-binding assay is provided, useful for screening libraries
CC   of synthetic or biological cpds. for their ability to bind DNA test
CC   sequences. The assay is versatile in that any number of test sequences
CC   can be tested by placing the test sequence adjacent to a defined protein-
CC   binding screening sequence. Binding of mols. to these test sequences
CC   changes the binding characteristics of the protein mol. to its cognate
CC   binding sequence. When such a mol. binds the test sequence, the
CC   equilibrium of the DNA:protein complexes is disturbed, generating changes
CC   in the concentration of free DNA probe. One application of this method is
CC   to eucaryotic general transcription factors (e.g. TFIID), where the
CC   target region is typically selected from DNA sequences adjacent to the
CC   binding site for the eucaryotic transcription factor. Numerous exemplary
CC   test sequences are given: the sequences in AAQ69251-731 and AAQ69850
CC   correspond to promoter targets (typically, TATA box-contg. sites) for
CC   human genes and the sequences in AAQ69732-849 correspond to promoter
CC   targets for viral genes. The test sequences may also be randomly
CC   generated. DNA:protein interaction may be used for screening purposes,
CC   e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see
CC   AAQ69851-52, AAQ69865 and AAQ69891). (Updated on 25-MAR-2003 to correct
CC   PN field.)
XX
SQ   Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;

Query Match   56.8%; Score 14.2; DB 2; Length 49;
Best Local Similarity   84.2%;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   7 GGGGCCTGGCCCCTTAATA 25
             ||||| ||| ||| |||| ||
Db   10 GGGGGCCCGGCCCGTTAAGA 28

XX

RESULT 10
ID   AAQ69655/c standard; DNA; 49 BP.
XX
AC   AAQ69655;
XX
DT   25-MAR-2003 (revised)
DT   01-MAR-1995 (first entry)

```
XX
DE   Human adenosine deaminase gene, target region.
XX
KW   DNA protein-binding assay; test sequence; screening sequence; promoter;
KW   target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9;
KW   transcription factor; TFIID; ds.
XX
OS   Synthetic.
XX
PN   WO9414980-A1.
XX
PD   07-JUL-1994.
XX
PF   20-DEC-1993;   93WO-US012388.
XX
PR   23-DEC-1992;   92US-0099678.
PR   17-SEP-1993;   93US-00123936.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;
XX
DR   WPI; 1994-234711/28.
XX
PT   Sequence-directed DNA-binding molecules - useful in pharmaceuticals and
PT   as molecular reagents.
XX
PS   Claim 28; Page 414; 587pp; English.
XX
CC   A DNA protein-binding assay is provided, useful for screening libraries
CC   of synthetic or biological cpds. for their ability to bind DNA test
CC   sequences. The assay is versatile in that any number of test sequences
CC   can be tested by placing the test sequence adjacent to a defined protein-
CC   binding sequence. Binding of mols. to these test sequences
CC   changes the binding characteristics of the protein mol. to its cognate
CC   binding sequence. When such a mol. binds the test sequence, the
CC   equilibrium of the DNA:protein complexes is disturbed, generating changes
CC   in the concentration of free DNA probe. One application of this method is
CC   to eucaryotic general transcription factors (e.g. TFIID), where the
CC   target region is typically selected from DNA sequences adjacent to the
CC   binding site for the eucaryotic transcription factor. Numerous exemplary
CC   test sequences are given: the sequences in AAQ69251-731 and AAQ69850
CC   correspond to promoter targets (typically, TATA box-contg. sites) for
CC   human genes and the sequences in AAQ69732-849 correspond to promoter
CC   targets for viral genes. The test sequences may also be randomly
CC   generated. DNA:protein interaction may be used for screening purposes,
CC   e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see
CC   AAQ69851-52; AAQ69865 and AAQ69891). (Updated on 25-MAR-2003 to correct
CC   PN field.)
XX
SQ   Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;

Query Match             56.8%;  Score 14.2;  DB 2;  Length 49;
Best Local Similarity   84.2%;
Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TATTAAGGGGCCTGGCCCC 19
              |||| |||||| ||||||
Db         28 TCTTAACGGGCCGGGGCCCC 10

RESULT 11
ID   AAT64117 standard; DNA; 49 BP.
XX
AC   AAT64117;
XX
DT   25-MAR-2003  (revised)
DT   17-MAR-1997  (first entry)
XX
DE   Human adenosine deaminase gene TFIID binding site.
XX
KW   Duplex DNA; target region; binding characteristic; DNA binding protein;
```

```
KW   TFIID; transcription factor; binding site; inhibition; enhance; cancer;
KW   inherited genetic disorder; ds.
XX
OS   Homo sapiens.
XX
PN   US5578444-A.
XX
PD   26-NOV-1996.
XX
PF   20-DEC-1993;   93US-00171389.
XX
PR   27-JUN-1991;   91US-00723618.
PR   23-DEC-1992;   92US-00996783.
PR   17-SEP-1993;   93US-00123936.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;
XX
DR   WPI; 1997-020402/02.
XX
PT   Altering binding characteristics of DNA binding proteins to duplex DNA -
PT   by attaching binding specific small cpd. to target region close to the protein's
PT   binding site, useful in treatment of viral disease, cancer etc.
XX
PS   Claim 6; Col 305-306; 264pp; English.
XX
CC   The sequences given in AAT63713-4312 represent duplex DNA's which act as
CC   target regions in the method of the invention. The method for altering
CC   the binding characteristics of a DNA-binding protein to duplex DNA
CC   comprises contacting the duplex DNA with a small molecule which binds
CC   sequence-specifically to a target region, where, when the small molecule
CC   is bound to the target region, it is adjacent to, but not overlapping by
CC   more than 4 bp, a binding site for a DNA-binding protein. The small
CC   molecule is added at a concentration effective to alter the binding of
CC   the DNA binding protein, pref. TFIID, to its binding site on the duplex
CC   DNA. The binding of the small molecule may inhibit or enhance the binding
CC   of the DNA-binding protein to its binding site. The compounds isolated
CC   using this method are potentially useful as therapeutic agents for
CC   treatment of any disease which involves a specific DNA sequence, e.g.
CC   cancer, or inherited genetic disorders etc. The method is suitable for
CC   screening large biological or chemical libraries and allows determination
CC   of sequence-specific and relative affinities of known DNA-binding agents
CC   for different DNA sequences. The design of these duplex DNA's allows a
CC   single DNA:protein interaction to be used for screening sequence-
CC   specific, or preferential, DNA binding proteins that recognise almost any
CC   possible sequence (see also AAT49539-74). (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;

Query Match             56.8%;  Score 14.2;  DB 2;  Length 49;
Best Local Similarity   84.2%;
Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 GGGGGCCTGGCGCCCCTTAATA 25
              ||||||| ||||| ||||
Db         10 GGGGGCCCGGCCCGGTTAAGA 28

RESULT 12
ID   AAT64117/c standard; DNA; 49 BP.
XX
AC   AAT64117;
XX
DT   25-MAR-2003  (revised)
DT   17-MAR-1997  (first entry)
XX
DE   Human adenosine deaminase gene TFIID binding site.
XX
KW   Duplex DNA; target region; binding characteristic; transcription factor; binding site; inhibition; enhance; cancer;
```

KW   Inherited genetic disorder; ds.
XX
OS   Homo sapiens.
XX
PN   US5578444-A.
XX
PD   26-NOV-1996.
XX
PP   20-DEC-1993;   93US-0017189.
XX
PR   27-JUN-1991;   91US-00723618.
PR   23-DEC-1992;   92US-0099683.
PR   17-SEP-1993;   93US-00123936.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;
XX
DR   WPI; 1997-020402/02.
XX
PT   Altering binding characteristics of DNA binding proteins to duplex DNA -
     by attaching specific small cpd. to target region close to the protein's
     binding site, useful in treatment of viral disease, cancer etc.
PS   Claim 6; Col 305-306; 264pp; English.
XX
CC   The sequences given in AAT63713-4312 represent duplex DNA's which act as
CC   target regions in the method of the invention. The method for altering
CC   the binding characteristics of a DNA-binding protein to duplex DNA
CC   comprises contacting the duplex DNA with a small molecule which binds
CC   sequence-specifically to a target region, where, when the small molecule
CC   is bound to the target region, it is adjacent to, but not overlapping by
CC   more than 4 bp, a binding protein. The small molecule
CC   is added at a concentration effective to alter the binding of
CC   the DNA binding protein, pref. TFIID, to its binding site on the duplex
CC   DNA. The binding of the small molecule may inhibit or enhance the binding
CC   of the DNA-binding protein to its binding site. The compounds isolated
CC   using this method are potentially useful as therapeutic agents for
CC   treatment of any disease which involves a specific DNA sequence, e.g.
CC   cancer, or inherited genetic disorders etc. The method is suitable for
CC   screening large biological or chemical libraries and allows determination
CC   of sequence-specific and relative affinities of known DNA-binding agents
CC   for different DNA sequences. The design of these duplex DNA's allows a
CC   single DNA:protein interaction to be used for screening sequence-
CC   specific, or preferential, DNA binding proteins that recognise almost any
CC   possible sequence (see also AAT49539-74). (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;

Query Match   56.8%; Score 14.2; DB 2; Length 49;
Best Local Similarity   84.2%;
Matches   16; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

```
Qy   1 TATTAAGGGGCCTGGCCCC 19
         |||| ||||| |||||||
Db  28 TCTTAACGGGCCCGGCCCC 10
```

RESULT 13
AAX17405
ID   AAX17405 standard; DNA; 49 BP.
XX
AC   AAX17405;
XX
DT   06-MAY-1999   (first entry)
XX
DE   Test sequence from human adenosine deaminase gene.
XX
KW   Test sequence; DNA-binding molecule; screening sequence; human;
KW   nucleic acid amplification; target; viral; ds.
XX
OS   Homo sapiens.

XX
PN   US5869241-A.
XX
PD   09-FEB-1999.
XX
PP   07-JUN-1995;   95US-0047528.
XX
PR   27-JUN-1991;   91US-00723618.
PR   23-DEC-1992;   92US-0099683.
PR   17-SEP-1993;   93US-00123936.
PR   20-DEC-1993;   93US-00171389.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fry KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;
XX
DR   WPI; 1999-152755/13.
XX
PT   Determination of DNA sequence preference of a DNA-binding molecule -
     based on inhibition of binding of protein to oligonucleotide sequence
     attached to test sequence.
PS   Claim 3; Col 307-308; 270pp; English.
XX
CC   Sequences AAX17001 to AAX17600 represent specifically claimed target test
CC   sequences that are used in the method of the invention of determining the
CC   DNA sequence preference of a DNA-binding molecule. The method comprises:
CC   (i) adding a test molecule and a DNA-binding protein to a mixture of
CC   duplex DNA test oligonucleotides, each of the test oligonucleotides
CC   having a test sequence adjacent to a screening sequence, where the
CC   screening sequence binds to the DNA-binding protein with a binding
CC   affinity that is independent of the DNA sequence of the test sequence,
CC   and where the mixture of duplex DNA test oligonucleotides includes
CC   several test sequences; (ii) incubating the test molecule, the mixture of
CC   duplex DNA test oligonucleotides and the DNA-binding protein for a time
CC   sufficient to permit binding of the test molecule to test sequences in
CC   the duplex DNA; (iii) separating unbound test oligonucleotides from test
CC   oligonucleotides bound to binding protein; (iv) amplifying the unbound
CC   test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating
CC   the amplified test oligonucleotides; and (vii) sequencing the isolated
CC   test oligonucleotides. Test sequences AAX17001-X17481 and AAX17600
CC   correspond to promoter targets for human genes and test sequences
CC   AAX17482-X17599 correspond to promoter targets for viral genes
XX
SQ   Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;

Query Match   56.8%; Score 14.2; DB 2; Length 49;
Best Local Similarity   84.2%;
Matches   16; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

```
Qy   7 GGGGCCTGGCCCCTTAATA 25
         |||||| |||| |||| ||
Db  10 GGGGCCCGGCCCGTTAAGA 28
```

RESULT 14
AAX17405/c
ID   AAX17405/c standard; DNA; 49 BP.
XX
AC   AAX17405;
XX
DT   06-MAY-1999   (first entry)
XX
DE   Test sequence from human adenosine deaminase gene.
XX
KW   Test sequence; DNA-binding molecule; screening sequence; human;
KW   nucleic acid amplification; target; viral; ds.
XX
OS   Homo sapiens.
XX
PN   US5869241-A.
XX
PD   09-FEB-1999.

XX
PF 07-JUN-1995;   95US-0047528.
XX
PR 27-JUN-1991;   91US-00723618.
PR 23-DEC-1992;   92US-0099678.3
PR 17-SEP-1993;   93US-0012393.6
PR 20-DEC-1993;   93US-00171389.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fry KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;
XX
DR WPI; 1999-152755/13.
XX
PT Determination of DNA sequence preference of a DNA-binding molecule - based on inhibition of binding of protein to oligonucleotide sequence attached to test sequence.
XX
PS Claim 3; Col 307-308; 270pp; English.
XX
CC Sequences AAX17001 to AAX17600 represent specifically claimed target test sequences that are used in the method of the invention of determining the DNA sequence preference of a DNA-binding molecule. The method comprises: (i) adding a test oligonucleotide, and a DNA-binding protein to a mixture of duplex DNA test oligonucleotides, each of the test oligonucleotides having a test sequence adjacent to a screening sequence, where the screening sequence binds to the DNA-binding protein with a binding affinity that is independent of the DNA sequence of the test sequence, and where the mixture of duplex DNA test oligonucleotides includes several test sequences; (ii) incubating the test molecule, the mixture of duplex DNA test oligonucleotides and the DNA-binding protein for a time sufficient to permit binding of the test molecule to test sequences in the duplex DNA; (iii) separating unbound test oligonucleotides from test oligonucleotides bound to binding protein; (iv) amplifying the unbound test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and (vii) sequencing the isolated test oligonucleotides. Test sequences AAX17001-X17481 and AAX17600 correspond to promoter targets for human genes and test sequences AAX17482-X17599 correspond to promoter targets for viral genes
XX
SQ Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;

Query Match   56.8%; Score 14.2; DB 2; Length 49;
Best Local Similarity   84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   1 TATTAAGGGGCCCTGGCCCC 19
        ||||| ||||||||||||
Db 28 TCTTAACGGGCCCGGCCCC 10

RESULT 15
ABK82896
ID ABK82896 standard; DNA; 49 BP.
XX
AC ABK82896;
XX
DT 27-AUG-2002 (first entry)
XX
DB DNA binding molecule screening method test sequence #405.
XX
KW DNA binding molecule screening; inhibition of transcription; infection; human immunodeficiency virus; HIV; parasite; cancer; cardiovascular; respiratory; gastrointestinal; endocrine; metabolic; rheumatic; immunological; haematological; neurological; psychiatric; dermatological; ophthalmological; musculo-skeletal; urogenital disorder; ss.
XX
OS Synthetic.
XX
PN US6384208-B1.
XX
PD 07-MAY-2002.
XX

XX
PF 15-JUL-1999;   99US-00354947.
XX
PR 27-JUN-1991;   91US-00723618.
PR 23-DEC-1992;   92US-00996783.
PR 17-SEP-1993;   93US-00123936.
PR 20-DEC-1993;   93US-00171389.
PR 07-JUN-1995;   95US-00482080.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;
XX
DR WPI; 2002-442819/47.
XX
PT Decreasing transcriptional activity of genes for treating infections or cancer, by administration of an agent that binds to two non-overlapping regions of the gene.
XX
PS Example 15; SEQ ID NO 405; 98pp; English.
XX
CC The invention relates to a method of decreasing transcriptional activity in a duplex deoxyribonucleic acid (DNA) template (T1) comprising contacting (T1) with a binding agent comprising at least one small duplex DNA-binding molecule (T2) coupled to at least one other small duplex-binding molecule that binds to a non-overlapping region of target sequence (TS). The method is useful for inhibiting transcription of a range of disease-related genes for treating infections (by viruses, including human immunodeficiency virus, bacteria, fungi, protozoa and parasites), cancer, cardiovascular, respiratory, gastrointestinal, endocrine/metabolic, rheumatic/immunological, haematological, neurological, psychiatric, dermatological, ophthalmological, musculo-skeletal, genetic or urogenital disorders. The method provides sequence-specific inhibition of transcription of pathological genes without affecting transcription of cellular genes regulated by the same transcription factor, and can be applied to regulation of any gene. ABK82492-ABK93155 represent DNA binding molecule test sequences used in the method of the invention
XX
SQ Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;

Query Match   56.8%; Score 14.2; DB 6; Length 49;
Best Local Similarity   84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   7 GGGGGCCTGGGCCCCTTAATA 25
        ||||||| |||| | ||
Db 10 GGGGGCCCGGGCCCGTTAAGA 28

Search completed: February 7, 2006, 13:57:24
Job time : 275 secs